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(54) Title: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

(57) Abstract

Nucleic acid molecules are isolated from *Sorangium cellulosum* that encode polypeptides necessary for the biosynthesis of epothilone. Disclosed are methods for the production of epothilone in recombinant hosts transformed with the genes of the invention. In this manner, epothilone can be produced in quantities large enough to enable their purification and use in pharmaceutical formulations such as those for the treatment of cancer.

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GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FIELD OF THE INVENTION

The present invention relates generally to polyketides and genes for their synthesis. In particular, the present invention relates to the isolation and characterization of novel polyketide synthase and nonribosomal peptide synthetase genes from *Sorangium cellulosum* that are necessary for the biosynthesis of epothilones A and B.

BACKGROUND OF THE INVENTION

Polyketides are compounds synthesized from two-carbon building blocks, the β-carbon of which always carries a keto group, thus the name polyketide. These compounds include many important antibiotics, immunosuppressants, cancer chemotherapeutic agents, and other compounds possessing a broad range of biological properties. The tremendous structural diversity derives from the different lengths of the polyketide chain, the different side-chains introduced (either as part of the two-carbon building blocks or after the polyketide backbone is formed), and the stereochemistry of such groups. The keto groups may also be reduced to hydroxyls, enoyls, or removed altogether. Each round of two-carbon addition is carried out by a complex of enzymes called the polyketide synthase (PKS) in a manner similar to fatty acid biosynthesis.

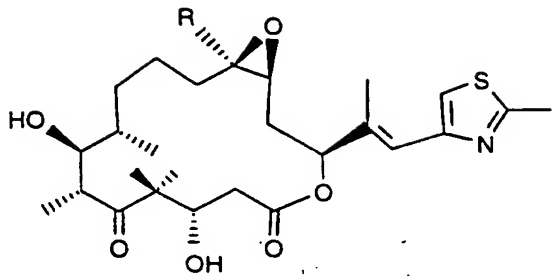
The biosynthetic genes for an increasing number of polyketides have been isolated and sequenced. For example, *see* U.S. Patent Nos. 5,639,949, 5,693,774, and 5,716,849, all of which are incorporated herein by reference, which describe genes for the biosynthesis of soraphen. *See also*, Schupp *et al.*, *FEMS Microbiology Letters* 159: 201-207 (1998) and WO 98/07868, which describe genes for the biosynthesis of rifamycin, and U.S. Patent No. 5,876,991, which describes genes for the biosynthesis of tylactone, all of which are incorporated herein by reference. The encoded proteins generally fall into two types: type I and type II. Type I proteins are polyfunctional, with several catalytic domains carrying out different enzymatic steps covalently linked together (e.g. PKS for erythromycin, soraphen, rifamycin, and avermectin (MacNeil *et al.*, in *Industrial Microorganisms: Basic and Applied Molecular Genetics*, (ed.: Baltz *et al.*), American Society for Microbiology, Washington D. C.

pp. 245-256 (1993)); whereas type II proteins are monofunctional (Hutchinson *et al.*, in *Industrial Microorganisms: Basic and Applied Molecular Genetics*, (ed.: Baltz *et al.*), American Society for Microbiology, Washington D. C. pp. 203-216 (1993)).

For the simpler polyketides such as actinorhodin (produced by *Streptomyces coelicolor*), the several rounds of two-carbon additions are carried out iteratively on PKS enzymes encoded by one set of PKS genes. In contrast, synthesis of the more complicated compounds such as erythromycin and soraphen involves PKS enzymes that are organized into modules, whereby each module carries out one round of two-carbon addition (for review, see Hopwood *et al.*, in *Industrial Microorganisms: Basic and Applied Molecular Genetics*, (ed.: Baltz *et al.*), American Society for Microbiology, Washington D. C., pp. 267-275 (1993)).

Complex polyketides and secondary metabolites in general may contain substructures that are derived from amino acids instead of simple carboxylic acids. Incorporations of these building blocks are accomplished by non-ribosomal polypeptide synthetases (NRPSs). NRPSs are multienzymes that are organized in modules. Each module is responsible for the addition (and the additional processing, if required) of one amino acid building block. NRPSs activate amino acids by forming aminoacyl-adenylates, and capture the activated amino acids on thiol groups of phophopantheteinyl prosthetic groups on peptidyl carrier protein domains. Further, NRPSs modify the amino acids by epimerization, N-methylation, or cyclization if necessary, and catalyse the formation of peptide bonds between the enzyme-bound amino acids. NRPSs are responsible for the biosynthesis of peptide secondary metabolites like cyclosporin, could provide polyketide chain terminator units as in rapamycin, or form mixed systems with PKSs as in yersiniabactin biosynthesis.

Epothilones A and B are 16-membered macrocyclic polyketides with an acylcysteine-derived starter unit that are produced by the bacterium *Sorangium cellulosum* strain So ce90 (Gerth *et al.*, *J. Antibiotics* 49: 560-563 (1996), incorporated herein by reference). The structure of epothilone A and B wherein R signifies hydrogen (epothilone A) or methyl (epothilone B) is:



The epothilones have a narrow antifungal spectrum and especially show a high cytotoxicity in animal cell cultures (*see*, Höfle *et al.*, Patent DE 4138042 (1993), incorporated herein by reference). Of significant importance, epothilones mimic the biological effects of taxol, both *in vivo* and in cultured cells (Bollag *et al.*, *Cancer Research* 55: 2325-2333 (1995), incorporated herein by reference). Taxol and taxotere, which stabilize cellular microtubules, are cancer chemotherapeutic agents with significant activity against various human solid tumors (Rowinsky *et al.*, *J. Natl. Cancer Inst.* 83: 1778-1781 (1991)). Competition studies have revealed that epothilones act as competitive inhibitors of taxol binding to microtubules, consistent with the interpretation that they share the same microtubule-binding site and possess a similar microtubule affinity as taxol. However, epothilones enjoy a significant advantage over taxol in that epothilones exhibit a much lower drop in potency compared to taxol against a multiple drug-resistant cell line (Bollag *et al.* (1995)). Furthermore, epothilones are considerably less efficiently exported from the cells by P-glycoprotein than is taxol (Gerth *et al.* (1996)). In addition, several epothilone analogs have been synthesized that have a superior cytotoxic activity as compared to epothilone A or epothilone B as demonstrated by their enhanced ability to induce the polymerization and stabilization of microtubules (WO 98/25929, incorporated herein by reference).

Despite the promise shown by the epothilones as anticancer agents, problems pertaining to the production of these compounds presently limit their commercial potential. The compounds are too complex for industrial-scale chemical synthesis and so must be produced by fermentation. Techniques for the genetic manipulation of myxobacteria such as *Sorangium cellulosum* are described in U.S. Patent No. 5,686,295, incorporated herein by reference. However, *Sorangium cellulosum* is notoriously difficult to ferment and production levels of epothilones are therefore low. Recombinant production of epothilones in heterologous hosts that are more amenable to fermentation could solve current production problems. However, the genes that encode the polypeptides responsible for epothilone bio-

synthesis have heretofore not been isolated. Furthermore, the strain that produces epothilones, i.e. So ce90, also produces at least one additional polyketide, spirangien, which would be expected to greatly complicate the isolation of the genes particularly responsible for epothilone biosynthesis.

Therefore, in view of the foregoing, one object of the present invention is to isolate the genes that are involved in the synthesis of epothilones, particularly the genes that are involved in the synthesis of epothilones A and B in myxobacteria of the Sorangium/-Polyangium group, i.e., *Sorangium cellulosum* strain So ce90. A further object of the invention is to provide a method for the recombinant production of epothilones for application in anticancer formulations.

SUMMARY OF THE INVENTION

In furtherance of the aforementioned and other objects, the present invention unexpectedly overcomes the difficulties set forth above to provide for the first time a nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of epothilone. In a preferred embodiment, the nucleotide sequence is isolated from a species belonging to *Myxobacteria*, most preferably *Sorangium cellulosum*.

In another preferred embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of an epothilone, wherein said polypeptide comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: SEQ ID NO:2, amino acids 11-437 of SEQ ID NO:2, amino acids 543-864 of SEQ ID NO:2, amino acids 974-1273 of SEQ ID NO:2, amino acids 1314-1385 of SEQ ID NO:2, SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, amino acids 1344-1351 of SEQ ID NO:3, SEQ ID NO:4, amino acids 7-432 of SEQ ID NO:4, amino acids 539-859 of SEQ ID NO:4, amino acids 869-1037 of SEQ ID NO:4, amino acids 1439-1684 of SEQ ID NO:4, amino acids 1722-1792 of SEQ ID

NO:4, SEQ ID NO:5, amino acids 39-457 of SEQ ID NO:5, amino acids 563-884 of SEQ ID NO:5, amino acids 1147-1399 of SEQ ID NO:5, amino acids 1434-1506 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 3886-4048 of SEQ ID NO:5, amino acids 4433-4719 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, SEQ ID NO:6, amino acids 35-454 of SEQ ID NO:6, amino acids 561-881 of SEQ ID NO:6, amino acids 1143-1393 of SEQ ID NO:6, amino acids 1430-1503 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, amino acids 2053-2373 of SEQ ID NO:6, amino acids 2383-2551 of SEQ ID NO:6, amino acids 2671-3045 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, SEQ ID NO:7, amino acids 32-450 of SEQ ID NO:7, amino acids 556-877 of SEQ ID NO:7, amino acids 887-1051 of SEQ ID NO:7, amino acids 1478-1790 of SEQ ID NO:7, amino acids 1810-2055 of SEQ ID NO:7, amino acids 2093-2164 of SEQ ID NO:7, amino acids 2165-2439 of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:22.

In a more preferred embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of an epothilone, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:2, amino acids 11-437 of SEQ ID NO:2, amino acids 543-864 of SEQ ID NO:2, amino acids 974-1273 of SEQ ID NO:2, amino acids 1314-1385 of SEQ ID NO:2, SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, amino acids 1344-1351 of SEQ ID NO:3, SEQ ID NO:4, amino acids 7-432 of SEQ ID NO:4, amino acids 539-859 of SEQ ID NO:4, amino acids 869-1037 of SEQ ID NO:4, amino acids 1439-1684

of SEQ ID NO:4, amino acids 1722-1792 of SEQ ID NO:4, SEQ ID NO:5, amino acids 39-457 of SEQ ID NO:5, amino acids 563-884 of SEQ ID NO:5, amino acids 1147-1399 of SEQ ID NO:5, amino acids 1434-1506 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 3886-4048 of SEQ ID NO:5, amino acids 4433-4719 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, SEQ ID NO:6, amino acids 35-454 of SEQ ID NO:6, amino acids 561-881 of SEQ ID NO:6, amino acids 1143-1393 of SEQ ID NO:6, amino acids 1430-1503 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, amino acids 2053-2373 of SEQ ID NO:6, amino acids 2383-2551 of SEQ ID NO:6, amino acids 2671-3045 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, SEQ ID NO:7, amino acids 32-450 of SEQ ID NO:7, amino acids 556-877 of SEQ ID NO:7, amino acids 887-1051 of SEQ ID NO:7, amino acids 1478-1790 of SEQ ID NO:7, amino acids 1810-2055 of SEQ ID NO:7, amino acids 2093-2164 of SEQ ID NO:7, amino acids 2165-2439 of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:22.

In yet another preferred embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of an epothilone, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: the complement of nucleotides 1900-3171 of SEQ ID NO:1, nucleotides 3415-5556 of SEQ ID NO:1, nucleotides 7610-11875 of SEQ ID NO:1, nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1,

nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, nucleotides 15901-15924 of SEQ ID NO:1, nucleotides 16251-21749 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 21746-43519 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 43524-54920 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, nucleotides 51534-52657 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, nucleotides 54935-62254 of SEQ ID NO:1, nucleotides 55028-56284 of SEQ ID NO:1, nucleotides 56600-57565 of SEQ ID NO:1, nucleotides 57593-58087 of SEQ ID NO:1, nucleotides 59366-60304 of SEQ ID NO:1, nucleotides 60362-61099 of SEQ ID NO:1, nucleotides 61211-61426 of SEQ ID NO:1, nucleotides 61427-62254 of SEQ ID NO:1, nucleotides 62369-63628 of SEQ ID NO:1, nucleotides 67334-68251 of SEQ ID NO:1, and nucleotides 1-68750 SEQ ID NO:1.

In an especially preferred embodiment, the present invention provides a nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of an epothilone, wherein said nucleotide sequence is selected from the group consisting of: the complement of nucleotides 1900-3171 of SEQ ID NO:1, nucleotides 3415-5556 of SEQ ID NO:1, nucleotides 7610-11875 of SEQ ID NO:1, nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 11872-16104 of

SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, nucleotides 15901-15924 of SEQ ID NO:1, nucleotides 16251-21749 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 21746-43519 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 43524-54920 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, nucleotides 51534-52657 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, nucleotides 54935-62254 of SEQ ID NO:1, nucleotides 55028-56284 of SEQ ID NO:1, nucleotides 56600-57565 of SEQ ID NO:1, nucleotides 57593-58087 of SEQ ID NO:1, nucleotides 59366-60304 of SEQ ID NO:1, nucleotides 60362-61099 of SEQ ID NO:1, nucleotides 61211-61426 of SEQ ID NO:1, nucleotides 61427-62254 of SEQ ID NO:1, nucleotides 62369-63628 of SEQ ID NO:1, nucleotides 67334-68251 of SEQ ID NO:1, and nucleotides 1-68750 SEQ ID NO:1.

In yet another preferred embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of an epothilone, wherein said nucleotide sequence comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: the complement of nucleotides 1900-3171 of SEQ ID NO:1, nucleotides 3415-5556 of SEQ ID NO:1, nucleotides 7610-11875 of SEQ ID NO:1, nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, nucleotides 15901-15924 of SEQ ID NO:1, nucleotides 16251-21749 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 21746-43519 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 43524-54920 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID

NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, nucleotides 51534-52657 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, nucleotides 54935-62254 of SEQ ID NO:1, nucleotides 55028-56284 of SEQ ID NO:1, nucleotides 56600-57565 of SEQ ID NO:1, nucleotides 57593-58087 of SEQ ID NO:1, nucleotides 59366-60304 of SEQ ID NO:1, nucleotides 60362-61099 of SEQ ID NO:1, nucleotides 61211-61426 of SEQ ID NO:1, nucleotides 61427-62254 of SEQ ID NO:1, nucleotides 62369-63628 of SEQ ID NO:1, nucleotides 67334-68251 of SEQ ID NO:1, and nucleotides 1-68750 SEQ ID NO:1.

The present invention also provides a chimeric gene comprising a heterologous promoter sequence operatively linked to a nucleic acid molecule of the invention. Further, the present invention provides a recombinant vector comprising such a chimeric gene, wherein the vector is capable of being stably transformed into a host cell. Still further, the present invention provides a recombinant host cell comprising such a chimeric gene, wherein the host cell is capable of expressing the nucleotide sequence that encodes at least one polypeptide necessary for the biosynthesis of an epothilone. In a preferred embodiment, the recombinant host cell is a bacterium belonging to the order *Actinomycetales*, and in a more preferred embodiment the recombinant host cell is a strain of *Streptomyces*. In other embodiments, the recombinant host cell is any other bacterium amenable to fermentation, such as a pseudomonad or *E. coli*. Even further, the present invention provides a Bac clone comprising a nucleic acid molecule of the invention, preferably Bac clone pEPO15.

In another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes an epothilone synthase domain.

According to one embodiment, the epothilone synthase domain is a β-ketoacyl-synthase (KS) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7. According to this embodiment, said KS domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids

3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, and nucleotides 55028-56284 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, and nucleotides 55028-56284 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, and nucleotides 55028-56284 of SEQ ID NO:1.

According to another embodiment, the epothilone synthase domain is an acyltransferase (AT) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7. According to this embodiment, said AT domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino

acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, and nucleotides 56600-57565 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, and nucleotides 56600-57565 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, and nucleotides 56600-57565 of SEQ ID NO:1.

According to still another embodiment, the epothilone synthase domain is an enoyl reductase (ER) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7. According to this embodiment, said ER domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 10529-11428 of

SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, and nucleotides 59366-60304 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, and nucleotides 59366-60304 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, and nucleotides 59366-60304 of SEQ ID NO:1.

According to another embodiment, the epothilone synthase domain is an acyl carrier protein (ACP) domain, wherein said polypeptide comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7. According to this embodiment, said ACP domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, and nucleotides 61211-61426 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40,

45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, and nucleotides 61211-61426 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, and nucleotides 61211-61426 of SEQ ID NO:1.

According to another embodiment, the epothilone synthase domain is a dehydratase (DH) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7. According to this embodiment, said DH domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, and nucleotides 57593-58087 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, and nucleotides 57593-58087 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 18855-19361 of SEQ ID NO:1,

nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, and nucleotides 57593-58087 of SEQ ID NO:1.

According to yet another embodiment, the epothilone synthase domain is a β-keto-reductase (KR) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7. According to this embodiment, said KR domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, and nucleotides 60362-61099 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, and nucleotides 60362-61099 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, and nucleotides 60362-61099 of SEQ ID NO:1.

According to an additional embodiment, the epothilone synthase domain is a methyltransferase (MT) domain comprising an amino acid sequence substantially similar to amino acids 2671-3045 of SEQ ID NO:6. According to this embodiment, said MT domain preferably comprises amino acids 2671-3045 of SEQ ID NO:6. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to nucleotides 51534-52657 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of nucleotides 51534-52657 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is nucleotides 51534-52657 of SEQ ID NO:1.

According to another embodiment, the epothilone synthase domain is a thioesterase (TE) domain comprising an amino acid sequence substantially similar to amino acids 2165-2439 of SEQ ID NO:7. According to this embodiment, said TE domain preferably comprises amino acids 2165-2439 of SEQ ID NO:7. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to nucleotides 61427-62254 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of nucleotides 61427-62254 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is nucleotides 61427-62254 of SEQ ID NO:1.

In still another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a non-ribosomal peptide synthetase, wherein said non-ribosomal peptide synthetase comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, and amino acids 1344-1351 of SEQ ID NO:3. According to this

embodiment, said non-ribosomal peptide synthetase preferably comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, and amino acids 1344-1351 of SEQ ID NO:3. Also, according to this embodiment, said nucleotide sequence preferably is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, and nucleotides 15901-15924 of SEQ ID NO:1. According to this embodiment, said nucleotide sequence more preferably comprises a consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair nucleotide portion identical in sequence to a respective consecutive 20, 25, 30, 35, 40, 45, or 50 (preferably 20) base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, and nucleotides 15901-15924 of SEQ ID NO:1. In addition, according to this embodiment, said nucleotide sequence most preferably is selected from the group consisting of: nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-

12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, and nucleotides 15901-15924 of SEQ ID NO:1.

The present invention further provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:2-23.

In accordance with another aspect, the present invention also provides methods for the recombinant production of polyketides such as epothilones in quantities large enough to enable their purification and use in pharmaceutical formulations such as those for the treatment of cancer. A specific advantage of these production methods is the chirality of the molecules produced; production in transgenic organisms avoids the generation of populations of racemic mixtures, within which some enantiomers may have reduced activity. In particular, the present invention provides a method for heterologous expression of epothilone in a recombinant host, comprising: (a) introducing into a host a chimeric gene comprising a heterologous promoter sequence operatively linked to a nucleic acid molecule of the invention that comprises a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of epothilone; and (b) growing the host in conditions that allow biosynthesis of epothilone in the host. The present invention also provides a method for producing epothilone, comprising: (a) expressing epothilone in a recombinant host by the aforementioned method; and (b) extracting epothilone from the recombinant host.

According to still another aspect, the present invention provides an isolated polypeptide comprising an amino acid sequence that consists of an epothilone synthase domain.

According to one embodiment, the epothilone synthase domain is a β-ketoacyl-synthase (KS) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7. According to this embodiment,

said KS domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7.

According to another embodiment, the epothilone synthase domain is an acyltransferase (AT) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7. According to this embodiment, said AT domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7.

According to still another embodiment, the epothilone synthase domain is an enoyl reductase (ER) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7. According to this embodiment, said ER domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7.

According to another embodiment, the epothilone synthase domain is an acyl carrier protein (ACP) domain, wherein said polypeptide comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of

SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7. According to this embodiment, said ACP domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7.

According to another embodiment, the epothilone synthase domain is a dehydratase (DH) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7. According to this embodiment, said DH domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7.

According to yet another embodiment, the epothilone synthase domain is a β-keto-reductase (KR) domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7. According to this embodiment, said KR domain preferably comprises an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7.

According to an additional embodiment, the epothilone synthase domain is a methyltransferase (MT) domain comprising an amino acid sequence substantially similar to amino acids 2671-3045 of SEQ ID NO:6. According to this embodiment, said MT domain preferably comprises amino acids 2671-3045 of SEQ ID NO:6.

According to another embodiment, the epothilone synthase domain is a thioesterase (TE) domain comprising an amino acid sequence substantially similar to amino acids 2165-2439 of SEQ ID NO:7. According to this embodiment, said TE domain preferably comprises amino acids 2165-2439 of SEQ ID NO:7.

Other aspects and advantages of the present invention will become apparent to those skilled in the art from a study of the following description of the invention and non-limiting examples.

DEFINITIONS

In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

Associated With / Operatively Linked: Refers to two DNA sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

Chimeric Gene: A recombinant DNA sequence in which a promoter or regulatory DNA sequence is operatively linked to, or associated with, a DNA sequence that codes for an mRNA or which is expressed as a protein, such that the regulator DNA sequence is able to regulate transcription or expression of the associated DNA sequence. The regulator DNA sequence of the chimeric gene is not normally operatively linked to the associated DNA sequence as found in nature.

Coding DNA Sequence: A DNA sequence that is translated in an organism to produce a protein.

Domain: That part of a polyketide synthase necessary for a given distinct activity. Examples include acyl carrier protein (ACP), β-ketosynthase (KS), acyltransferase (AT), β-ketoreductase (KR), dehydratase (DH), enoylreductase (ER), and thioesterase (TE) domains.

Epothilones: 16-membered macrocyclic polyketides naturally produced by the bacterium *Sorangium cellulosum* strain So ce90, which mimic the biological effects of taxol. In this application, "epothilone" refers to the class of polyketides that includes epothilone A and epothilone B, as well as analogs thereof such as those described in WO 98/25929.

Epothilone Synthase: A polyketide synthase responsible for the biosynthesis of epothilone.

Gene: A defined region that is located within a genome and that, besides the aforementioned coding DNA sequence, comprises other, primarily regulatory, DNA sequences responsible for the control of the expression, that is to say the transcription and translation, of the coding portion.

Heterologous DNA Sequence: A DNA sequence not naturally associated with a host cell into which it is introduced, including non-naturally occurring multiple copies of a naturally occurring DNA sequence.

Homologous DNA Sequence: A DNA sequence naturally associated with a host cell into which it is introduced.

Homologous Recombination: Reciprocal exchange of DNA fragments between homologous DNA molecules.

Isolated: In the context of the present invention, an isolated nucleic acid molecule or an isolated enzyme is a nucleic acid molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated nucleic acid molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, a recombinant host cell.

Module: A genetic element encoding all of the distinct activities required in a single round of polyketide biosynthesis, i.e., one condensation step and all the β-carbonyl processing steps associated therewith. Each module encodes an ACP, a KS, and an AT activity to accomplish the condensation portion of the biosynthesis, and selected post-condensation activities to effect the β-carbonyl processing.

NRPS: A non-ribosomal polypeptide synthetase, which is a complex of enzymatic activities responsible for the incorporation of amino acids into secondary metabolites including, for example, amino acid adenylation, epimerization, N-methylation, cyclization, peptidyl carrier protein, and condensation domains. A functional NRPS is one that catalyzes the incorporation of an amino acid into a secondary metabolite.

NRPS gene: One or more genes encoding NRPSs for producing functional secondary metabolites, e.g., epothilones A and B, when under the direction of one or more compatible control elements.

Nucleic Acid Molecule: A linear segment of single- or double-stranded DNA or RNA that can be isolated from any source. In the context of the present invention, the nucleic acid molecule is preferably a segment of DNA.

ORF: Open Reading Frame.

PKS: A polyketide synthase, which is a complex of enzymatic activities (domains) responsible for the biosynthesis of polyketides including, for example, ketoreductase, dehydratase, acyl carrier protein, enoylreductase, ketoacyl ACP synthase, and acyltransferase. A functional PKS is one that catalyzes the synthesis of a polyketide.

PKS Genes: One or more genes encoding various polypeptides required for producing functional polyketides, e.g., epothilones A and B, when under the direction of one or more compatible control elements.

Substantially Similar: With respect to nucleic acids, a nucleic acid molecule that has at least 60 percent sequence identity with a reference nucleic acid molecule. In a preferred embodiment, a substantially similar DNA sequence is at least 80% identical to a reference DNA sequence; in a more preferred embodiment, a substantially similar DNA sequence is at least 90% identical to a reference DNA sequence; and in a most preferred embodiment, a substantially similar DNA sequence is at least 95% identical to a reference DNA sequence. A substantially similar DNA sequence preferably encodes a protein or peptide having substantially the same activity as the protein or peptide encoded by the reference DNA sequence. A substantially similar nucleotide sequence typically hybridizes to a reference nucleic acid molecule, or fragments thereof, under the following conditions: hybridization at 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$ pH 7.0, 1 mM EDTA at 50°C; wash with 2X SSC, 1% SDS, at 50°C. With respect to proteins or peptides, a substantially similar amino acid sequence is an amino acid sequence that is at least 90% identical to the amino acid sequence of a reference protein or peptide and has substantially the same activity as the reference protein or peptide.

Transformation: A process for introducing heterologous nucleic acid into a host cell or organism.

Transformed / Transgenic / Recombinant: Refers to a host organism such as a bacterium into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to

encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed", "non-transgenic", or "non-recombinant" host refers to a wild-type organism, i.e., a bacterium, which does not contain the heterologous nucleic acid molecule.

Nucleotides are indicated by their bases by the following standard abbreviations: adenine (A), cytosine (C), thymine (T), and guanine (G). Amino acids are likewise indicated by the following standard abbreviations: alanine (ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C), glutamine (Gln; Q), glutamic acid (Glu; E), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V). Furthermore, (Xaa; X) represents any amino acid.

DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

SEQ ID NO:1 is the nucleotide sequence of a 68750 bp contig containing 22 open reading frames (ORFs), which comprises the epothilone biosynthesis genes.

SEQ ID NO:2 is the protein sequence of a type I polyketide synthase (EPOS A) encoded by *epo*A (nucleotides 7610-11875 of SEQ ID NO:1).

SEQ ID NO:3 is the protein sequence of a non-ribosomal peptide synthetase (EPOS P) encoded by *epo*P (nucleotides 11872-16104 of SEQ ID NO:1).

SEQ ID NO:4 is the protein sequence of a type I polyketide synthase (EPOS B) encoded by *epo*B (nucleotides 16251-21749 of SEQ ID NO:1).

SEQ ID NO:5 is the protein sequence of a type I polyketide synthase (EPOS C) encoded by *epo*C (nucleotides 21746-43519 of SEQ ID NO:1).

SEQ ID NO:6 is the protein sequence of a type I polyketide synthase (EPOS D) encoded by *epo*D (nucleotides 43524-54920 of SEQ ID NO:1).

SEQ ID NO:7 is the protein sequence of a type I polyketide synthase (EPOS E) encoded by *epo*E (nucleotides 54935-62254 of SEQ ID NO:1).

SEQ ID NO:8 is the protein sequence of a cytochrome P450 oxygenase homologue (EPOS F) encoded by *epo*F (nucleotides 62369-63628 of SEQ ID NO:1).

SEQ ID NO:9 is a partial protein sequence (partial Orf 1) encoded by *orf*1 (nucleotides 1-1826 of SEQ ID NO:1).

SEQ ID NO:10 is a protein sequence (Orf 2) encoded by *orf*2 (nucleotides 3171-1900 on the reverse complement strand of SEQ ID NO:1).

SEQ ID NO:11 is a protein sequence (Orf 3) encoded by *orf*3 (nucleotides 3415-5556 of SEQ ID NO:1).

SEQ ID NO:12 is a protein sequence (Orf 4) encoded by *orf*4 (nucleotides 5992-5612 on the reverse complement strand of SEQ ID NO:1).

SEQ ID NO:13 is a protein sequence (Orf 5) encoded by *orf*5 (nucleotides 6226-6675 of SEQ ID NO:1).

SEQ ID NO:14 is a protein sequence (Orf 6) encoded by *orf*6 (nucleotides 63779-64333 of SEQ ID NO:1).

SEQ ID NO:15 is a protein sequence (Orf 7) encoded by *orf*7 (nucleotides 64290-63853 on the reverse complement strand of SEQ ID NO:1).

SEQ ID NO:16 is a protein sequence (Orf 8) encoded by *orf*8 (nucleotides 64363-64920 of SEQ ID NO:1).

SEQ ID NO:17 is a protein sequence (Orf 9) encoded by *orf*9 (nucleotides 64727-64287 on the reverse complement strand of SEQ ID NO:1).

SEQ ID NO:18 is a protein sequence (Orf 10) encoded by *orf*10 (nucleotides 65063-65767 of SEQ ID NO:1).

SEQ ID NO:19 is a protein sequence (Orf 11) encoded by *orf*11 (nucleotides 65874-65008 on the reverse complement strand of SEQ ID NO:1).

SEQ ID NO:20 is a protein sequence (Orf 12) encoded by *orf*12 (nucleotides 66338-65871 on the reverse complement strand of SEQ ID NO:1).

SEQ ID NO:21 is a protein sequence (Orf 13) encoded by *orf*13 (nucleotides 66667-67137 of SEQ ID NO:1).

SEQ ID NO:22 is a protein sequence (Orf 14) encoded by *orf*14 (nucleotides 67334-68251 of SEQ ID NO:1).

SEQ ID NO:23 is a partial protein sequence (partial Orf 15) encoded by *orf*15 (nucleotides 68346-68750 of SEQ ID NO:1).

SEQ ID NO:24 is the universal reverse PCR primer sequence.

SEQ ID NO:25 is the universal forward PCR primer sequence.

SEQ ID NO:26 is the NH24 end "B" PCR primer sequence.

SEQ ID NO:27 is the NH2 end "A" PCR primer sequence.

SEQ ID NO:28 is the NH2 end "B" PCR primer sequence.

SEQ ID NO:29 is the pEPO15-NH6 end "B" PCR primer sequence.
SEQ ID NO:30 is the pEPO15-H2.7 end "A" PCR primer sequence.

DEPOSIT INFORMATION

The following material has been deposited with the Agricultural Research Service, Patent Culture Collection (NRRL), 1815 North University Street, Peoria, Illinois 61604, under the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. All restrictions on the availability of the deposited material will be irrevocably removed upon the granting of a patent.

Deposited Material	Accession Number	Deposit Date
pEPO15	NRRL B-30033	June 11, 1998
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DETAILED DESCRIPTION OF THE INVENTION

The genes involved in the biosynthesis of epothilones can be isolated using the techniques according to the present invention. The preferable procedure for the isolation of epothilone biosynthesis genes requires the isolation of genomic DNA from an organism identified as producing epothilones A and B, and the transfer of the isolated DNA on a suitable plasmid or vector to a host organism that does not normally produce the polyketide, followed by the identification of transformed host colonies to which the epothilone-producing ability has been conferred. Using a technique such as λ::Tn5 transposon mutagenesis (de Bruijn & Lupski, *Gene* 27: 131-149 (1984)), the exact region of the transforming epothilone-conferring DNA can be more precisely defined. Alternatively or additionally, the transforming epothilone-conferring DNA can be cleaved into smaller fragments and the smallest that maintains the epothilone-conferring ability further characterized. Whereas the host organism lacking the ability to produce epothilone may be a different species from the organism from which the polyketide derives, a variation of this technique involves the transformation of host DNA into the same host that has had its epothilone-producing ability disrupted by mutagenesis. In this method, an epothilone-producing organism is mutated and non-epothilone-producing mutants are isolated. These are then complemented by genomic DNA isolated from the epothilone-producing parent strain.

A further example of a technique that can be used to isolate genes required for epothilone biosynthesis is the use of transposon mutagenesis to generate mutants of an epothilone-producing organism that, after mutagenesis, fails to produce the polyketide. Thus, the region of the host genome responsible for epothilone production is tagged by the transposon and can be recovered and used as a probe to isolate the native genes from the parent strain. PKS genes that are required for the synthesis of polyketides and that are similar to known PKS genes may be isolated by virtue of their sequence homology to the biosynthetic genes for which the sequence is known, such as those for the biosynthesis of rifamycin or soraphen. Techniques suitable for isolation by homology include standard library screening by DNA hybridization.

Preferred for use as a probe molecule is a DNA fragment that is obtainable from a gene or another DNA sequence that plays a part in the synthesis of a known polyketide. A preferred probe molecule comprises a 1.2 kb *Sma*I DNA fragment encoding the ketosynthase domain of the fourth module of the soraphen PKS (U.S. Patent No. 5,716,849), and a more preferred probe molecule comprises the β-ketoacyl synthase domains from the first and second modules of the rifamycin PKS (Schupp *et al.*, *FEMS Microbiology Letters* 159: 201-207 (1998)). These can be used to probe a gene library of an epothilone-producing microorganism to isolate the PKS genes responsible for epothilone biosynthesis.

Despite the well-known difficulties with PKS gene isolation in general and despite the difficulties expected to be encountered with the isolation of epothilone biosynthesis genes in particular, by using the methods described in the instant specification, biosynthetic genes for epothilones A and B can surprisingly be cloned from a microorganism that produces that polyketide. Using the methods of gene manipulation and recombinant production described in this specification, the cloned PKS genes can be modified and expressed in transgenic host organisms.

The isolated epothilone biosynthetic genes can be expressed in heterologous hosts to enable the production of the polyketide with greater efficiency than might be possible from native hosts. Techniques for these genetic manipulations are specific for the different available hosts and are known in the art. For example, heterologous genes can be expressed in *Streptomyces* and other actinomycetes using techniques such as those described in McDaniel *et al.*, *Science* 262: 1546-1550 (1993) and Kao *et al.*, *Science* 265: 509-512 (1994), both of which are incorporated herein by reference. *See also*, Rowe *et al.*, *Gene*

216: 215-223 (1998); Holmes *et al.*, *EMBO Journal* 12(8): 3183-3191 (1993) and Bibb *et al.*, *Gene* 38: 215-226 (1985), all of which are incorporated herein by reference.

Alternately, genes responsible for polyketide biosynthesis, i.e., epothilone biosynthetic genes, can also be expressed in other host organisms such as pseudomonads and *E. coli.* Techniques for these genetic manipulations are specific for the different available hosts and are known in the art. For example, PKS genes have been sucessfully expressed in *E. coli* using the pT7-7 vector, which uses the T7 promoter. *See*, Tabor *et al.*, *Proc. Natl. Acad. Sci. USA* 82: 1074-1078 (1985), incorporated herein by reference. In addition, the expression vectors pKK223-3 and pKK223-2 can be used to express heterologous genes in *E. coli,* either in transcriptional or translational fusion, behind the *tac or trc* promoter. For the expression of operons encoding multiple ORFs, the simplest procedure is to insert the operon into a vector such as pKK223-3 in transcriptional fusion, allowing the cognate ribosome binding site of the heterologous genes to be used. Techniques for overexpression in gram-positive species such as *Bacillus* are also known in the art and can be used in the context of this invention (Quax *et al.*, in: *Industrial Microorganisms: Basic and Applied Molecular Genetics, Eds.* Baltz *et al.*, American Society for Microbiology, Washington (1993)).

Other expression systems that may be used with the epothilone biosynthetic genes of the invention include yeast and baculovirus expression systems. See, for example, "The Expression of Recombinant Proteins in Yeasts," Sudbery, P. E., *Curr. Opin. Biotechnol.* 7(5): 517-524 (1996); "Methods for Expressing Recombinant Proteins in Yeast," Mackay, et al., Editor(s): Carey, Paul R., *Protein Eng. Des.* 105-153, Publisher: Academic, San Diego, Calif (1996); "Expression of heterologous gene products in yeast," Pichuantes, et al., Editor(s): Cleland, J. L., Craik, C. S., *Protein Eng.* 129-161, Publisher: Wiley-Liss, New York, N. Y (1996); WO 98/27203; Kealey *et al.*, *Proc. Natl. Acad. Sci. USA* 95: 505-509 (1998); "Insect Cell Culture: Recent Advances, Bioengineering Challenges And Implications In Protein Production," Palomares, et al., Editor(s): Galindo, Enrique; Ramirez, Octavio T., *Adv. Bioprocess Eng.* Vol. II, Invited Pap. Int. Symp., 2nd (1998) 25-52, Publisher: Kluwer, Dordrecht, Neth; "Baculovirus Expression Vectors," Jarvis, Donald L., Editor(s): Miller, Lois K., *Baculoviruses* 389-431, Publisher: Plenum, New York, N. Y. (1997); "Production Of Heterologous Proteins Using The Baculovirus/Insect Expression System," Grittiths, et al., *Methods Mol. Biol.* (Totowa, N. J.) 75 (Basic Cell Culture Protocols (2nd Edition)) 427-440 (1997); and "Insect Cell Expression Technology," Luckow, Verne A., *Protein Eng.* 183-218,

Publisher: Wiley-Liss, New York, N. Y. (1996); all of which are incorporated herein by reference.

Another consideration for expression of PKS genes in heterologous hosts is the requirement of enzymes for posttranslational modification of PKS enzymes by phosphopantetheinylation before they can synthesize polyketides. However, the enzymes responsible for this modification of type I PKS enzymes, phosphopantetheinyl (P-pant) transferases are not normally present in many hosts such as *E. coli*. This problem can be solved by coexpression of a P-pant transferase with the PKS genes in the heterologous host, as described by Kealey *et al., Proc. Natl. Acad. Sci. USA* 95: 505-509 (1998), incorporated herein by reference.

Therefore, for the purposes of polyketide production, the significant criteria in the choice of host organism are its ease of manipulation, rapidity of growth (*i.e.* fermentation), possession or the proper molecular machinery for processes such as posttranslational modification, and its lack of susceptibility to the polyketide being overproduced. Most preferred host organisms are actinomycetes such as strains of *Streptomyces*. Other preferred host organisms are pseudomonads and *E. coli*. The above-described methods of polyketide production have significant advantages over the technology currently used in the preparation of the compounds. These advantages include the cheaper cost of production, the ability to produce greater quantities of the compounds, and the ability to produce compounds of a preferred biological enantiomer, as opposed to racemic mixtures inevitably generated by organic synthesis. Compounds produced by heterologous hosts can be used in medical (*e.g.* cancer treatment in the case of epothilones) as well as agricultural applications.

EXPERIMENTAL

The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified. Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Ausubel (ed.), *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. (1994); T. Maniatis, E. F. Fritsch and J. Sambrook, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor laboratory, Cold Spring Harbor, NY (1989); and by T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984).

Example 1: Cultivation of an Epothilone-Producing Strain of *Sorangium cellulosum*

Sorangium cellulosum strain 90 (DSM 6773, Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig) is streaked out and grown (30°C) on an agar plate of SolE medium (0.35% glucose, 0.05% tryptone, 0.15% $MgSO_4 \times 7H_2O$, 0.05% ammonium sulfate, 0.1% $CaCl_2$, 0.006% K_2HPO_4, 0.01% sodium dithionite, 0.0008% Fe-EDTA, 1.2% HEPES, 3.5% [vol/vol] supernatant of sterilized stationary *S. cellulosum* culture) pH ad. 7.4. Cells from about 1 square cm are picked and inoculated into 5 mls of G51t liquid medium (0.2% glucose, 0.5% starch, 0.2% tryptone, 0.1% probion S, 0.05% $CaCl_2x2H_20$, 0.05% $MgSO_4x7H_20$, 1.2% HEPES, pH ad. 7.4) and incubated at 30°C with shaking at 225 rpm. After 4 days, the culture is transferred into 50 mls of G51t and incubated as above for 5 days. This culture is used to inoculate 500 mls of G51t and incubated as above for 6 days. The culture is centrifuged for 10 minutes at 4000 rpm and the cell pellet is resuspended in 50 mls of G51t.

Example 2: Generation of a Bacterial Artificial Chromosome (Bac) Library

To generate a Bac library, *S. cellulosum* cells cultivated as described in Example 1 above are embedded into agarose blocks, lysed, and the liberated genomic DNA is partially digested by the restriction enzyme *Hin*dIII. The digested DNA is separated on an agarose gel by pulsed-field electrophoresis. Large (approximately 90-150 kb) DNA fragments are

isolated from the agarose gel and ligated into the vector pBelobacII. pBelobacII contains a gene encoding chloramphenicol resistance, a multiple cloning site in the *lacZ* gene providing for blue/white selection on appropriate medium, as well as the genes required for the replication and maintenance of the plasmid at one or two copies per cell. The ligation mixture is used to transform *Escherichia coli* DH10B electrocompetent cells using standard electroporation techniques. Chloramphenicol-resistant recombinant (white, *lacZ* mutant) colonies are transferred to a positively charged nylon membrane filter in 384 3X3 grid format. The clones are lysed and the DNA is cross-linked to the filters. The same clones are also preserved as liquid cultures at -80°C.

Example 3: Screening the Bac Library of *Sorangium cellulosum* 90 for the Presence of Type I Polyketide Synthase-Related Sequences

The Bac library filters are probed by standard Southern hybridization procedures. The DNA probes used encode β-ketoacyl synthase domains from the first and second modules of the rifamycin polyketide synthase (Schupp *et al., FEMS Microbiology Letters* 159: 201-207 (1998)). The probe DNAs are generated by PCR with primers flanking each ketosynthase domain using the plasmid pNE95 as the template (pNE95 equals cosmid 2 described in Schupp et al. (1998)). 25 ng of PCR-amplified DNA is isolated from a 0.5% agarose gel and labeled with ^{32}P-dCTP using a random primer labeling kit (Gibco-BRL, Bethesda MD, USA) according to the manufacturer's instructions. Hybridization is at 65°C for 36 hours and membranes are washed at high stringency (3 times with 0.1x SSC and 0.5% SDS for 20 min at 65°C). The labeled blot is exposed on a phosphorescent screen and the signals are detected on a PhospholmageR 445SI (screen and 445SI from Molecular Dynamics). This results in strong hybridization of certain Bac clones to the probes. These clones are selected and cultured overnight in 5 mls of Luria broth (LB) at 37°C. Bac DNA from the Bac clones of interest is isolated by a typical miniprep procedure. The cells are resuspended in 200 µl lysozyme solution (50mM glucose, 10 mM EDTA, 25 mM Tris-HCl, 5mg/ml lysozyme), lysed in 400 µl lysis solution (0.2 N NaOH and 2% SDS), the proteins are precipitated (3.0 M potassium acetate, adjusted to pH5.2 with acetic acid), and the Bac DNA is precipitated with isopropanol. The DNA is resuspended in 20µl of nuclease-free distilled water, restricted with *Bam*HI (New England Biolabs, Inc.) and separated on a 0.7% agarose gel. The gel is blotted by Southern hybridization as described above and probed

under conditions described above, with a 1.2 kb *Sma*I DNA fragment encoding the ketosynthase domain of the fourth module of the soraphen polyketide synthase as the probe (*see*, U.S. Patent No. 5,716,849). Five different hybridization patterns are observed. One clone representing each of the five patterns is selected and named pEPO15, pEPO20, pEPO30, pEPO31, and pEPO33, respectively.

Example 4: Subcloning of *Bam*HI Fragments from pEPO15, pEPO20, pEPO30, pEPO31, and pEPO33

The DNA of the five selected Bac clones is digested with *Bam*HI and random fragments are subcloned into pBluescript II SK+ (Stratagene) at the *Bam*HI site. Subclones carrying inserts between 2 and 10 kb in size are selected for sequencing of the flanking ends of the inserts and also probed with the 1.2 *Sma*I probe as described above. Subclones that show a high degree of sequence homology to known polyketide synthases and/or strong hybridization to the soraphen ketosynthase domain are used for gene disruption experiments.

Example 5: Preparation of Streptomycin-Resistant Spontaneous Mutants of *Sorangium cellulosum* strain So ce90

0.1 ml of a three day old culture of *Sorangium cellulosum* strain So ce90, which is raised in liquid medium G52-H (0.2% yeast extract, 0.2% soyameal defatted, 0.8% potato starch, 0.2% glucose, 0.1% MgSO4 x7H2O, 0.1% CaCl2 x2H2O, 0.008% Fe-EDTA, pH ad 7.4 with KOH), is plated out on agar plates with SolE medium supplemented with 100 µg/ml streptomycin. The plates are incubated at 30°C for 2 weeks. The colonies growing on this medium are streptomycin-resistant mutants, which are streaked out and cultivated once more on the same agar medium with streptomycin for purification. One of these streptomycin-resistant mutants is selected and is called BCE28/2.

Example 6: Gene Disruptions in *Sorangium cellulosum* BCE28/2 Using the Subcloned *Bam*HI Fragments

The *Bam*HI inserts of the subclones generated from the five selected Bac clones as described above are isolated and ligated into the unique *Bam*HI site of plasmid pCIB132 (*see*, U.S. Patent No. 5,716,849). The pCIB132 derivatives carrying the inserts are transformed into Escherichia coli ED8767 containing the helper plasmid pUZ8 (Hedges and Matthew, *Plasmid* 2: 269-278 (1979). The transformants are used as donors in conjugation experiments with *Sorangium cellulosum* BCE28/2 as recipient. For the conjugation, 5-10 x 10^9 cells of *Sorangium cellulosum* BCE28/2 from an early stationary phase culture (reaching about 5 x 10^8 cells/ml) grown at 30°C in liquid medium G51b (G51b equals medium G51t with tryptone replaced by peptone) are mixed in a 1:1 cellular ratio with a late-log phase culture (in LB liquid medium) of *E. coli* ED8767 containing pCIB132 derivatives carrying the subcloned *Bam*HI fragments and the helper plasmid pUZ8. The mixed cells are then centrifuged at 4000 rpm for 10 minutes and resuspended in 0.5 ml G51b medium. This cell suspension is then plated as a drop in the center of a plate with So1E agar containg 50 mg/l kanamycin. The cells obtained after incubation for 24 hours at 30°C are harvested and resuspended in 0.8 ml of G51b medium, and 0.1 to 0.3 ml of this suspension is plated out on a selective So1E solid medium containing phleomycin (30 mg/l), streptomycin (300 mg/l), and kanamycin (50 mg/l). The counterselection of the donor *Escherichia coli* strain takes place with the aid of streptomycin. The colonies that grow on this selective medium after an incubation time of 8-12 days at a temperature of 30°C are isolated with a plastic loop and streaked out and cultivated on the same agar medium for a second round of selection and purification. The colony-derived cultures that grow on this selective agar medium after 7 days at a temperature of 30°C are transconjugants of *Sorangium cellulosum* BCE28/2 that have acquired phleomycin resistance by conjugative transfer of the pCIB132 derivatives carrying the subcloned *Bam*HI fragments.

Integration of the pCIB132-derived plasmids into the chromosome of *Sorangium cellulosum* BCE28/2 by homologous recombination is verified by Southern hybridization. For this experiment, complete DNA from 5-10 tranconjugants per transferred *Bam*HI fragment is isolated (from 10 ml cultures grown in medium G52-H for three days) applying the method described by Pospiech and Neumann, *Trends Genet.* 11: 217 (1995). For the Southern blot, the DNA isolated as described above is cleaved either with the restriction

enzymes *Bgl*II, *Cla*I, or *Not*I, and the respective *Bam*HI inserts or pCIB132 are used as 32P labelled probes.

Example 7: Analysis of the Effect of the Integrated *Bam*HI Fragments on Epothilone Production by *Sorangium cellulosum* After Gene Disruption

Transconjugant cells grown on about 1 square cm surface of the selective So1E plates of the second round of selection (see Example 6) are transferred by a sterile plastic loop into 10 ml of medium G52-H in an 50 ml Erlenmeyer flask. After incubation at 30°C and 180 rpm for 3 days, the culture is transfered into 50 ml of medium G52-H in an 200 ml Erlenmeyer flask. After incubation at 30°C and 180 rpm for 4-5 days, 10 ml of this culture is transfered into 50 ml of medium 23B3 (0.2 % glucose, 2 % potato starch, 1.6 % soya meal defatted, 0.0008 % Fe-EDTA Sodium salt, 0.5 % HEPES (4-(2-hydroxyethyl)-piperazine-1-ethane-sulfonic-acid), 2 % vol/vol polysterole resin XAD16 (Rohm & Haas), pH adjusted to 7.8 with NaOH) in an 200 ml Erlenmeyer flask.

Quantitative determination of the epothilone produced takes place after incubation of the cultures at 30°C and 180 rpm for 7 days. The complete culture broth is filtered by suction through a 150 µm nylon filter. The resin remaining on the filter is then resuspended in 10 ml isopropanol and extracted by shaking the suspension at 180 rpm for 1 hour. 1 ml is removed from this suspension and centrifuged at 12,000 rpm in an Eppendorff Microfuge. The amount of epothilones A and B therein is determined by means of an HPLC and detection at 250 nm with a UV_DAD detector (HPLC with Waters -Symetry C18 column and a gradient of 0.02 % phosphoric acid 60%-0% and acetonitril 40%-100%).

Transconjugants with three different integrated *Bam*HI fragments subcloned from pEPO15, namely transconjugants with the *Bam*HI fragment of plasmid pEPO15-21, transconjugants with the *Bam*HI fragment of plasmid pEPO15-4-5, and transconjugants with the *Bam*HI fragment of plasmid pEPO15-4-1, are tested in the manner described above. HPLC analysis reveals that all transconjugants no longer produce epothilone A or B. By contrast, epothilone A and B are detectable in a concentration of 2-4 mg/l in transconjugants with *Bam*HI fragments integrated that are derived from pEPO20, pEPO30, pEPO31, pEPO33, and in the parental strain BCE28/2.

Example 8: Nucleotide Sequence Determination of the Cloned Fragments and Construction of Contigs

A. *Bam*HI Insert of Plasmid pEPO15-21

Plasmid DNA is isolated from the strain *Escherichia coli* DH10B [pEPO15-21], and the nucleotide sequence of the 2.3-kb *Bam*HI insert in pEPO15-21 is determined. Automated DNA sequencing is done on the double-stranded DNA template by the dideoxynucleotide chain termination method, using Applied Biosystems model 377 sequencers. The primers used are the universal reverse primer (5' GGA AAC AGC TAT GAC CAT G 3' (SEQ ID NO:24)) and the universal forward primer (5' GTA AAA CGA CGG CCA GT 3' (SEQ ID NO:25)). In subsequent rounds of sequencing reactions, custom-synthesized oligonucleotides, designed for the 3' ends of the previously determined sequences, are used to extend and join contigs. Both strands are entirely sequenced, and every nucleotide is sequenced at least two times. The nucleotide sequence is compiled using the program Sequencher vers. 3.0 (Gene Codes Corporation), and analyzed using the University of Wisconsin Genetics Computer Group programs. The nucleotide sequence of the 2213-bp insert corresponds to nucleotides 20779-22991 of SEQ ID NO:1.

B. *Bam*HI Insert of Plasmid pEPO15-4-1

Plasmid DNA is isolated from the strain *Escherichia coli* DH10B [pEPO15-4-1], and the nucleotide sequence of the 3.9-kb *Bam*HI insert in pEPO15-4-1 is determined as described in (A) above. The nucleotide sequence of the 3909-bp insert corresponds to nucleotides 16876-20784 of SEQ ID NO:1.

C. *Bam*HI Insert of Plasmid pEPO15-4-5

Plasmid DNA is isolated from the strain *Escherichia coli* DH10B [pEPO15-4-5], and the nucleotide sequence of the 2.3-kb *Bam*HI insert in pEPO15-4-5 is determined as described in (A) above. The nucleotide sequence of the 2233-bp insert corresponds to nucleotides 42528-44760 of SEQ ID NO:1.

Example 9: Subcloning and Ordering of DNA Fragments from pEPO15 Containing Epothilone Biosynthesis Genes

pEPO15 is digested to completion with the restriction enzyme *Hin*dIII and the resulting fragments are subcloned into pBluescript II SK- or pNEB193 (New England Biolabs) that has been cut with *Hin*dIII and dephosphorylated with calf intestinal alkaline phosphatase. Six different clones are generated and named pEPO15-NH1, pEPO15-NH2, pEPO15-NH6, pEPO15-NH24 (all based on pNEB193), and pEPO15-H2.7 and pEPO15-H3.0 (both based on pBluescript II SK-).

The *Bam*HI insert of pEPO15-21 is isolated and DIG-labeled (Non-radioactive DNA labeling and detection system, Boehringer Mannheim), and used as a probe in DNA hybridization experiments at high stringency against pEPO15-NH1, pEPO15-NH2, pEPO15-NH6, pEPO15-NH24, pEPO15-H2.7 and pEPO15-H3.0. Strong hybridization signal is detected for pEPO15-NH24, indicating that pEPO15-21 is contained within pEPO15-NH24.

The *Bam*HI insert of pEPO15-4-1 is isolated and DIG-labeled as above, and used as a probe in DNA hybridization experiments at high stringency against pEPO15-NH1, pEPO15-NH2, pEPO15-NH6, pEPO15-NH24, pEPO15-H2.7 and pEPO15-H3.0. Strong hybridization signals are detected for pEPO15-NH24 and pEPO15-H2.7. Nucleotide sequence data generated from one end each of pEPO15-NH24 and pEPO15-H2.7 are also in complete agreement with the previously determined sequence of the *Bam*HI insert of pEPO15-4-1. These experiments demonstrate that pEPO15-4-1 (which contains one internal *Hin*dIII site) overlaps pEPO15-H2.7 and pEPO15-NH24, and that pEPO15-H2.7 and pEPO15-NH24, in this order, are contiguous.

The *Bam*HI insert of pEPO15-4-5 is isolated and DIG-labeled as above, and used as a probe in DNA hybridization experiments at high stringency against pEPO15-NH1, pEPO15-NH2, pEPO15-NH6, pEPO15-NH24, pEPO15-H2.7 and pEPO15-H3.0. Strong hybridization signal is detected for pEPO15-NH2, indicating that pEPO15-21 is contained within pEPO15-NH2.

Nucleotide sequence data is generated from both ends of pEPO15-NH2 and from the end of pEPO15-NH24 that does not overlap with pEPO15-4-1. PCR primers NH24 end "B": GTGACTGGCGCCTGGAATCTGCATGAGC (SEQ ID NO:26), NH2 end "A": AGCGGGAGCTTGCTAGACATTCTGTTTC (SEQ ID NO:27), and NH2 end "B": GACGCGCCTCGGGCAGCGCCCCAA (SEQ ID NO:28), pointing towards the *Hin*dIII sites,

are designed based on these sequences and used in amplification reactions with pEPO15 and, in separate experiments, with *Sorangium cellulosum* So ce90 genomic DNA as the templates. Specific amplification is found with primer pair NH24 end "B" and NH2 end "A" with both templates. The amplimers are cloned into pBluescript II SK- and completely sequenced. The sequences of the amplimers are identical, and also agree completely with the end sequences of pEPO15-NH24 and pEPO15-NH2, fused at the *Hin*dIII site, establishing that the *Hin*dIII fragments of pEPO15-NH2 and pEPO15-NH24 are, in this order, contiguous.

The *Hin*dIII insert of pEPO15-H2.7 is isolated and DIG-labeled as above, and used as a probe in a DNA hybridization experiment at high stringency against pEPO15 digested by *Not*I. A *Not*I fragment of about 9 kb in size shows a strong a hybridization, and is further subcloned into pBluescript II SK- that has been digested with *Not*I and dephosphorylated with calf intestinal alkaline phosphatase, to yield pEPO15-N9-16. The *Not*I insert of pEPO15-N9-16 is isolated and DIG-labeled as above, and used as a probe in DNA hybridization experiments at high stringency against pEPO15-NH1, pEPO15-NH2, pEPO15-NH6, pEPO15-NH24, pEPO15-H2.7 and pEPO15-H3.0. Strong hybridization signals are detected for pEPO15-NH6, and also for the expected clones pEPO15-H2.7 and pEPO15-NH24. Nucleotide sequence data is generated from both ends of pEPO15-NH6 and from the end of pEPO15-H2.7 that does not overlap with pEPO15-4-1. PCR primers are designed pointing towards the *Hin*dIII sites and used in amplification reactions with pEPO15 and, in separate experiments, with *Sorangium cellulosum* So ce90 genomic DNA as the templates. Specific amplification is found with primer pair pEPO15-NH6 end "B": CACCGAAGCGTCGATCTGGTCCATC (SEQ ID NO:29) and pEPO15-H2.7 end "A": CGGTCAGATCGACGACGGGCTTTCC (SEQ ID NO:30) with both templates. The amplimers are cloned into pBluescript II SK- and completely sequenced. The sequences of the amplimers are identical, and also agree completely with the end sequences of pEPO15-NH6 and pEPO15-H2.7, fused at the *Hin*dIII site, establishing that the *Hin*dIII fragments of pEPO15-NH6 and pEPO15-H2.7 are, in this order, contiguous.

All of these experiments, taken together, establish a contig of *Hin*dIII fragments covering a region of about 55 kb and consisting of the *Hin*dIII inserts of pEPO15-NH6, pEPO15-H2.7, pEPO15-NH24, and pEPO15-NH2, in this order. The inserts of the remaining two *Hin*dIII subclones, namely pEPO15-NH1 and pEPO15-H3.0, are not found to be parts of this contig.

Example 10: Further Extension of the Subclone Contig Covering the Epothilone Biosynthesis Genes

An approximately 2.2 kb *Bam*HI – *Hin*dIII fragment derived from the downstream end of the insert of pEPO15-NH2 and thus representing the downstream end of the subclone contig described in Example 9 is isolated, DIG-labeled, and used in Southern hybridization experiments against pEPO15 and pEPO15-NH2 DNAs digested with several enzymes. The strongly hybridizing bands are always found to be the same in size between the two target DNAs indicating that the *Sorangium cellulosum* So ce90 genomic DNA fragment cloned into pEPO15 ends with the *Hin*dIII site at the downstream end of pEPO15-NH2.

A cosmid DNA library of *Sorangium cellulosum* So ce90 is generated, using established procedures, in pScosTriplex-II (Ji, *et al., Genomics* 31: 185-192 (1996)). Briefly, high-molecular weight genomic DNA of *Sorangium cellulosum* So ce90 is partially digested with the restriction enzyme *Sau*3AI to provide fragments with average sizes of about 40 kb, and ligated to *Bam*HI and *Xba*I digested pScosTriplex-II. The ligation mix is packaged with Gigapack III XL (Stratagene) and used to transfect *E. coli* XL1 Blue MR cells.

The cosmid library is screened with the approximately 2.2 kb *Bam*HI – *Hin*dIII fragment, derived from the downstream end of the insert of pEPO15-NH2, used as a probe in colony hybridization. A strongly hybridizing clone, named pEPO4E7 is selected.

pEPO4E7 DNA is isolated, digested with several restriction endonucleases, and probed in Southern hybridization experiments with the 2.2 kb *Bam*HI – *Hin*dIII fragment. A strongly hybridizing *Not*I fragment of approximately 9 kb in size is selected and subcloned into pBluescript II SK- to yield pEPO4E7-N9-8. Further Southern hybridization experiments reveal that the approximately 9 kb *Not*I insert of pEPO4E7-N9-8 overlaps pEPO15-NH2 over 6 kb in a *Not*I – *Hin*dIII fragment, while the remaining approximately 3 kb *Hin*dIII – *Not*I fragment would extend the subclone contig described in Example 9. End sequencing reveals, however, that the downstream end of the insert of pEPO4E7-N9-8 contains the *Bam*HI – *Not*I polylinker of pScosTriplex-II, thereby indicating that the genomic DNA insert of pEPO4E7 ends at a *Sau*3AI site within the extending *Hin*dIII – *Not*I fragment and that the *Not*I site is derived from pScosTriplex-II.

An approximately 1.6 kb *Pst*I – *Sal*I fragment derived from the approximately 3 kb extending *Hin*dIII – *Not*I subfragment of pEPO4E7-N9-8, containing only *Sorangium*

cellulosum So ce90–derived sequences free of vector, is used as a probe against the bacterial artificial chromosome library described in Example 2. Besides the previously-isolated EPO15, a Bac clone, named EPO32, is found to strongly hybridize to the probe. pEPO32 is isolated, digested with several restriction endonucleases, and hybridized with the approximately 1.6 kb *Pst*I – *Sal*I probe. A *Hin*dIII – *Eco*RV fragment of about 13 kb in size is found to strongly hybridize to the probe, and is subcloned into pBluescript II SK- digested with *Hin*dIII and *Hin*cII to yield pEPO32-HEV15.

Oligonucleotide primers are designed based on the downstream end sequence of pEPO15-NH2 and on the upstream (*Hin*dIII) end sequence derived from pEPO32-HEV15, and used in sequencing reactions with pEPO4E7-N9-8 as the template. The sequences reveal the existence of a small *Hin*dIII fragment (EPO4E7-H0.02) of 24 bp, undetectable in standard restriction analysis, separating the *Hin*dIII site at the downstream end of pEPO15-NH2 from the *Hin*dIII site at the upstream end of pEPO32-HEV15.

Thus, the subclone contig described in Example 9 is extended to include the *Hin*dIII fragment EPO4E7-H0.02 and the insert of pEPO32-HEV15, and constitutes the inserts of: pEPO15-NH6, pEPO15-H2.7, pEPO15-NH24, pEPO15-NH2, EPO4E7-H0.02 and pEPO32-HEV15, in this order.

Example 11: Nucleotide Sequence Determination of the Subclone Contig Covering the Epothilone Biosynthesis Genes

The nucleotide sequence of the subclone contig described in Example 10 is determined as follows.

pEPO15-H2.7. Plasmid DNA is isolated from the strain *Escherichia coli* DH10B [pEPO15-H2.7], and the nucleotide sequence of the 2.7-kb *Bam*HI insert in pEPO15-H2.7 is determined. Automated DNA sequencing is done on the double-stranded DNA template by the dideoxynucleotide chain termination method, using Applied Biosystems model 377 sequencers. The primers used are the universal reverse primer (5' GGA AAC AGC TAT GAC CAT G 3' (SEQ ID NO:24)) and the universal forward primer (5' GTA AAA CGA CGG CCA GT 3' (SEQ ID NO:25)). In subsequent rounds of sequencing reactions, custom-synthesized oligonucleotides, designed for the 3' ends of the previously determined sequences, are used to extend and join contigs.

pEPO15-NH6, pEPO15-NH24 and pEPO15-NH2. The *Hind*III inserts of these plasmids are isolated, and subjected to random fragmentation using a Hydroshear apparatus (Genomic Instrumentation Services, Inc.) to yield an average fragment size of 1-2 kb. The fragments are end-repaired using T4 DNA Polymerase and Klenow DNA Polymerase enzymes in the presence of desoxynucleotide triphosphates, and phosphorylated with T4 DNA Kinase in the presence of ribo-ATP. Fragments in the size range of 1.5-2.2 kb are isolated from agarose gels, and ligated into pBluescript II SK- that has been cut with *Eco*RV and dephosphorylated. Random subclones are sequenced using the universal reverse and the universal forward primers.

pEPO32-HEV15. pEPO32-HEV15 is digested with *Hind*III and *Ssp*I, the approximately 13.3 kb fragment containing the ~13 kb *Hind*III – *Eco*RV insert from *So. cellulosum* So ce90 and a 0.3 kb *Hin*cII – *Ssp*I fragment from pBluescript II SK- is isolated, and partially digested with *Hae*III to yield fragments with an average size of 1-2 kb. Fragments in the size range of 1.5-2.2 kb are isolated from agarose gels, and ligated into pBluescript II SK- that has been cut with *Eco*RV and dephosphorylated. Random subclones are sequenced using the universal reverse and the universal forward primers.

The chromatograms are analyzed and assembled into contigs with the Phred, Phrap and Consed programs (Ewing, *et al., Genome Res.* 8(3): 175-185 (1998); Ewing, *et al., Genome Res.* 8(3): 186-194 (1998); Gordon, *et al., Genome Res.* 8(3): 195-202 (1998)). Contig gaps are filled, sequence discrepancies are resolved, and low-quality regions are resequenced using custom-designed oligonucleotide primers for sequencing on either the original subclones or selected clones from the random subclone libraries. Both strands are completely sequenced, and every basepair is covered with at least a minimum aggregated Phred score of 40 (confidence level of 99.99%).

The nucleotide sequence of the 68750 bp contig is shown as SEQ ID NO:1.

Example 12: Nucleotide Sequence Analysis of the Epothilone Biosynthesis Genes

SEQ ID NO:1 is found to contain 22 ORFs as detailed below in Table 1:

Table 1

ORF	Start codon	Stop codon	Homology of deduced protein	Proposed function of deduced protein
orf1	outside of sequenced range	1826		
orf2 *	3171	1900	Hypothetical protein SP: Q11037; DD-peptidase SP:P15555	
orf3	3415	5556	*Na/H antiporter PID: D1017724*	*Transport*
orf4 *	5992	5612		
orf5	6226	6675		
epoA	7610	11875	Type I polyketide synthase	Epothilone synthase: Thiazole ring formation
epoP	11872	16104	Non-ribosomal peptide synthetase	Epothilone synthase: Thiazole ring formation
epoB	16251	21749	Type I polyketide synthase	Epothilone synthase: Polyketide backbone formation
epoC	21746	43519	Type I polyketide synthase	Epothilone synthase: Polyketide backbone formation
epoD	43524	54920	Type I polyketide synthase	Epothilone synthase: Polyketide backbone formation
epoE	54935	62254	Type I polyketide synthase	Epothilone synthase: Polyketide backbone formation
epoF	62369	63628	Cytochrome P450	Epothilone macrolactone oxidase
orf6	63779	64333		
orf7 *	64290	63853		
orf8	64363	64920		
orf9 *	64727	64287		
orf10	65063	65767		
orf11 *	65874	65008		
orf12 *	66338	65871		
orf13	66667	67137		
orf14	67334	68251	Hypothetical protein GI:3293544; Cation efflux system protein GI:2623026	Transport
orf15	68346	outside of sequenced range		

* On the reverse complementer strand. Numbering according to SEQ ID NO:1.

epoA (nucleotides 7610-11875 of SEQ ID NO:1) codes for EPOS A (SEQ ID NO:2), a type I polyketide synthase consisting of a single module, and harboring the following domains: β-ketoacyl-synthase (KS) (nucleotides 7643-8920 of SEQ ID NO:1, amino acids 11-

437 of SEQ ID NO:2); acyltransferase (AT) (nucleotides 9236-10201 of SEQ ID NO:1, amino acids 543-864 of SEQ ID NO:2); enoyl reductase (ER) (nucleotides 10529-11428 of SEQ ID NO:1, amino acids 974-1273 of SEQ ID NO:2); and acyl carrier protein homologous domain (ACP) (nucleotides 11549-11764 of SEQ ID NO:1, amino acids 1314-1385 of SEQ ID NO:2). Sequence comparisons and motif analysis (Haydock, et al. *FEBS Lett.* 374: 246-248 (1995); Tang, et al., *Gene* 216: 255-265 (1998)) reveal that the AT encoded by EPOS A is specific for malonyl-CoA. EPOS A should be involved in the initiation of epothilone biosynthesis by loading the acetate unit to the multienzyme complex that will eventually form part of the 2-methylthiazole ring (C26 and C20).

*epo*P (nucleotides 11872-16104 of SEQ ID NO:1) codes for EPOS P (SEQ ID NO:3), a non-ribosomal peptide synthetase containing one module. EPOS P harbors the following domains:

- peptide bond formation domain, as delineated by motif K (amino acids 72-81 [FPLTDIQESY] of SEQ ID NO:3, corresponding to nucleotide positions 12085-12114 of SEQ ID NO:1); motif L (amino acids 118-125 [VVARHDML] of SEQ ID NO:3, corresponding to nucleotide positions 12223-12246 of SEQ ID NO:1); motif M (amino acids 199-212 [SIDLINVDLGSLSI] of SEQ ID NO:3, corresponding to nucleotide positions 12466-12507 of SEQ ID NO:1); and motif O (amino acids 353-363 [GDFTSMVLLDI] of SEQ ID NO:3, corresponding to nucleotide positions 12928-12960 of SEQ ID NO:1);
- aminoacyl adenylate formation domain, as delineated by motif A (amino acids 549-565 [LTYEELSRRSRRLGARL] of SEQ ID NO:3, corresponding to nucleotide positions 13516-13566 of SEQ ID NO:1); motif B (amino acids 588-603 [VAVLAVLESGAAYVPI] of SEQ ID NO:3, corresponding to nucleotide positions 13633-13680 of SEQ ID NO:1); motif C (amino acids 669-684 [AYVIYTSGSTGLPKGV] of SEQ ID NO:3, corresponding to nucleotide positions 13876-13923 of SEQ ID NO:1); motif D (amino acids 815-821 [SLGGATE] of SEQ ID NO:3, corresponding to nucleotide positions 14313-14334 of SEQ ID NO:1); motif E (amino acids 868-892 [GQLYIGGVGLALGYWRDEEKTRKSF] of SEQ ID NO:3, corresponding to nucleotide positions 14473-14547 of SEQ ID NO:1); motif F (amino acids 903-912 [YKTGDLGRYL] of SEQ ID NO:3, corresponding to nucleotide positions 14578-14607 of SEQ ID NO:1); motif G (amino acids 918-940 [EFMGREDNQIKLRGYRVELGEIE] of SEQ ID NO:3, corresponding to nucleotide positions 14623-14692 of SEQ ID NO:1); motif H (amino acids 1268-1274 [LPEYMVP] of SEQ ID NO:3, corresponding to nucleotide positions 15673-15693 of SEQ ID NO:1); and

motif I (amino acids 1285-1297 [LTSNGKVDRKALR] of SEQ ID NO:3, corresponding to nucleotide positions 15724-15762 of SEQ ID NO:1);

- an unknown domain, inserted between motifs G and H of the aminoacyl adenylate formation domain (amino acids 973-1256 of SEQ ID NO:3, corresponding to nucleotide positions 14788-15639 of SEQ ID NO:1); and
- a peptidyl carrier protein homologous domain (PCP), delineated by motif J (amino acids 1344-1351 [GATSIHIV] of SEQ ID NO:3, corresponding to nucleotide positions 15901-15924 of SEQ ID NO:1).

It is proposed that EPOS P is involved in the activation of a cysteine by adenylation, binding the activated cysteine as an aminoacyl-S-PCP, forming a peptide bond between the enzyme-bound cysteine and the acetyl-S-ACP supplied by EPOS A, and the formation of the initial thiazoline ring by intramolecular heterocyclization. The unknown domain of EPOS P displays very weak homologies to NAD(P)H oxidases and reductases from Bacillus species. Thus, this unknown domain and/or the ER domain of EPOS A may be involved in the oxidation of the initial 2-methylthiazoline ring to a 2-methylthiazole.

*epo*B (nucleotides 16251-21749 of SEQ ID NO:1) codes for EPOS B (SEQ ID NO:4), a type I polyketide synthase consisting of a single module, and harboring the following domains: KS (nucleotides 16269-17546 of SEQ ID NO:1, amino acids 7-432 of SEQ ID NO:4); AT (nucleotides 17865-18827 of SEQ ID NO:1, amino acids 539-859 of SEQ ID NO:4); dehydratase (DH) (nucleotides 18855-19361 of SEQ ID NO:1, amino acids 869-1037 of SEQ ID NO:4); β-ketoreductase (KR) (nucleotides 20565-21302 of SEQ ID NO:1, amino acids 1439-1684 of SEQ ID NO:4); and ACP (nucleotides 21414-21626 of SEQ ID NO:1, amino acids 1722-1792 of SEQ ID NO:4). Sequence comparisons and motif analysis reveal that the AT encoded by EPOS B is specific for methylmalonyl-CoA. EPOS A should be involved in the first polyketide chain extension by catalysing the Claisen-like condensation of the 2-methyl-4-thiazolecarboxyl-S-PCP starter group with the methylmalonyl-S-ACP, and the concomitant reduction of the b-keto group of C17 to an enoyl.

*epo*C (nucleotides 21746-43519 of SEQ ID NO:1) codes for EPOS C (SEQ ID NO:5), a type I polyketide synthase consisting of 4 modules. The first module harbors a KS (nucleotides 21860-23116 of SEQ ID NO:1, amino acids 39-457 of SEQ ID NO:5); a malonyl CoA-specific AT (nucleotides 23431-24397 of SEQ ID NO:1, amino acids 563-884 of SEQ ID NO:5); a KR (nucleotides 25184-25942 of SEQ ID NO:1, amino acids 1147-1399 of SEQ ID NO:5); and an ACP (nucleotides 26045-26263 of SEQ ID NO:1, amino acids 1434-1506 of

SEQ ID NO:5). This module incorporates an acetate extender unit (C14-C13) and reduces the β-keto group at C15 to the hydroxyl group that takes part in the final lactonization of the epothilone macrolactone ring. The second module of EPOS C harbors a KS (nucleotides 26318-27595 of SEQ ID NO:1, amino acids 1524-1950 of SEQ ID NO:5); a malonyl CoA-specific AT (nucleotides 27911-28876 of SEQ ID NO:1, amino acids 2056-2377 of SEQ ID NO:5); a KR (nucleotides 29678-30429 of SEQ ID NO:1, amino acids 2645-2895 of SEQ ID NO:5); and an ACP (nucleotides 30539-30759 of SEQ ID NO:1, amino acids 2932-3005 of SEQ ID NO:5). This module incorporates an acetate extender unit (C12-C11) and reduces the β-keto group at C13 to a hydroxyl group. Thus, the nascent polyketide chain of epothilone corresponds to epothilone A, and the incorporation of the methyl side chain at C12 in epothilone B would require a post-PKS C-methyltransferase activity. The formation of the epoxi ring at C13-C12 would also require a post-PKS oxidation step. The third module of EPOS C harbors a KS (nucleotides 30815-32092 of SEQ ID NO:1, amino acids 3024-3449 of SEQ ID NO:5); a malonyl CoA-specific AT (nucleotides 32408-33373 of SEQ ID NO:1, amino acids 3555-3876 of SEQ ID NO:5); a DH (nucleotides 33401-33889 of SEQ ID NO:1, amino acids 3886-4048 of SEQ ID NO:5); an ER (nucleotides 35042-35902 of SEQ ID NO:1, amino acids 4433-4719 of SEQ ID NO:5); a KR (nucleotides 35930-36667 of SEQ ID NO:1, amino acids 4729-4974 of SEQ ID NO:5); and an ACP (nucleotides 36773-36991 of SEQ ID NO:1, amino acids 5010-5082 of SEQ ID NO:5). This module incorporates an acetate extender unit (C10-C9) and fully reduces the β-keto group at C11. The fourth module of EPOS C harbors a KS (nucleotides 37052-38320 of SEQ ID NO:1, amino acids 5103-5525 of SEQ ID NO:5); a methylmalonyl CoA-specific AT (nucleotides 38636-39598 of SEQ ID NO:1, amino acids 5631-5951 of SEQ ID NO:5); a DH (nucleotides 39635-40141 of SEQ ID NO:1, amino acids 5964-6132 of SEQ ID NO:5); an ER (nucleotides 41369-42256 of SEQ ID NO:1, amino acids 6542-6837 of SEQ ID NO:5); a KR (nucleotides 42314-43048 of SEQ ID NO:1, amino acids 6857-7101 of SEQ ID NO:5); and an ACP (nucleotides 43163-43378 of SEQ ID NO:1, amino acids 7140-7211 of SEQ ID NO:5). This module incorporates a propionate extender unit (C24 and C8-C7) and fully reduces the β-keto group at C9.

*epo*D (nucleotides 43524-54920 of SEQ ID NO:1) codes for EPOS D (SEQ ID NO:6), a type I polyketide synthase consisting of 2 modules. The first module harbors a KS (nucleotides 43626-44885 of SEQ ID NO:1, amino acids 35-454 of SEQ ID NO:6); a methylmalonyl CoA-specific AT (nucleotides 45204-46166 of SEQ ID NO:1, amino acids 561-881 of SEQ ID NO:6); a KR (nucleotides 46950-47702 of SEQ ID NO:1, amino acids

1143-1393 of SEQ ID NO:6); and an ACP (nucleotides 47811-48032 of SEQ ID NO:1, amino acids 1430-1503 of SEQ ID NO:6). This module incorporates a propionate extender unit (C23 and C6-C5) and reduces the β-keto group at C7 to a hydoxyl group. The second module harbors a KS (nucleotides 48087-49361 of SEQ ID NO:1, amino acids 1522-1946 of SEQ ID NO: 6); a methylmalonyl CoA-specific AT (nucleotides 49680-50642 of SEQ ID NO:1, amino acids 2053-2373 of SEQ ID NO:6); a DH (nucleotides 50670-51176 of SEQ ID NO:1, amino acids 2383-2551 of SEQ ID NO:6); a methyltransferase (MT, nucleotides 51534-52657 of SEQ ID NO:1, amino acids 2671-3045 of SEQ ID NO:6); a KR (nucleotides 53697-54431 of SEQ ID NO:1, amino acids 3392-3636 of SEQ ID NO:6); and an ACP (nucleotides 54540-54758 of SEQ ID NO:1, amino acids 3673-3745 of SEQ ID NO:6). This module incorporates a propionate extender unit (C21 or C22 and C4-C3) and reduces the β-keto group at C5 to a hydoxyl group. This reduction is somewhat unexpected, since epothilones contain a keto group at C5. Discrepancies of this kind between the deduced reductive capabilities of PKS modules and the redox state of the corresponding positions in the final polyketide products have been, however, reported in the literature (see, for example, Schwecke, et al., *Proc. Natl. Acad. Sci. USA* 92: 7839-7843 (1995) and Schupp, et al., *FEMS Microbiology Letters* 159: 201-207 (1998)). An important feature of epothilones is the presence of gem-methyl side groups at C4 (C21 and C22). The second module of EPOS D is predicted to incorporate a propionate unit into the growing polyketide chain, providing one methyl side chain at C4. This module also contains a methyltransferase domain integrated into the PKS between the DH and the KR domains, in an arrangement similar to the one seen in the HMWP1 yersiniabactin synthase (Gehring, A.M., DeMoll, E., Fetherston, J.D., Mori, I., Mayhew, G.F., Blattner, F.R., Walsh, C.T., and Perry, R.D.: Iron acquisition in plague: modular logic in enzymatic biogenesis of yersiniabactin by Yersinia pestis. *Chem. Biol.* 5, 573-586, 1998). This MT domain in EPOS D is proposed to be responsible for the incorporation of the second methyl side group (C21 or C22) at C4.

*epo*E (nucleotides 54935-62254 of SEQ ID NO:1) codes for EPOS E (SEQ ID NO:7), a type I polyketide synthase consisting of one module, harboring a KS (nucleotides 55028-56284 of SEQ ID NO:1, amino acids 32-450 of SEQ ID NO:7); a malonyl CoA-specific AT (nucleotides 56600-57565 of SEQ ID NO:1, amino acids 556-877 of SEQ ID NO:7); a DH (nucleotides 57593-58087 of SEQ ID NO:1, amino acids 887-1051 of SEQ ID NO:7); a probably nonfunctional ER (nucleotides 59366-60304 of SEQ ID NO:1, amino acids 1478-1790 of SEQ ID NO:7); a KR (nucleotides 60362-61099 of SEQ ID NO:1, amino acids 1810-2055

of SEQ ID NO:7); an ACP (nucleotides 61211-61426 of SEQ ID NO:1, amino acids 2093-2164 of SEQ ID NO:7); and a thioesterase (TE) (nucleotides 61427-62254 of SEQ ID NO:1, amino acids 2165-2439 of SEQ ID NO:7). The ER domain in this module harbors an active site motif with some highly unusual amino acid substitutions that probably render this domain inactive. The module incorporates an acetate extender unit (C2-C1), and reduces the β-keto at C3 to an enoyl group. Epothilones contain a hydroxyl group at C3, so this reduction also appears to be excessive as discussed for the second module of EPOS D. The TE domain of EPOS E takes part in the release and cyclization of the grown polyketide chain via lactonization between the carboxyl group of C1 and the hydroxyl group of C15.

Five ORFs are detected upstream of *epo*A in the sequenced region. The partially sequenced *orf*1 has no homologues in the sequence databanks. The deduced protein product (Orf 2, SEQ ID NO:10) of *orf*2 (nucleotides 3171-1900 on the reverse complement strand of SEQ ID NO:1) shows strong similarities to hypothetical ORFs from *Mycobacterium* and *Streptomyces coelicolor*, and more distant similarities to carboxypeptidases and DD-peptidases of different bacteria. The deduced protein product of *orf*3 (nucleotides 3415-5556 of SEQ ID NO:1), Orf 3 (SEQ ID NO:11), shows homologies to Na/H antiporters of different bacteria. Orf 3 might take part in the export of epothilones from the producer strain. *orf*4 and *orf*5 have no homologues in the sequence databanks.

Eleven ORFs are found downstream of *epo*E in the sequenced region. *epo*F (nucleotides 62369-63628 of SEQ ID NO:1) codes for EPOS F (SEQ ID NO:8), a deduced protein with strong sequence similarities to cytochrome P450 oxygenases. EPOS F may take part in the adjustment of the redox state of the carbons C12, C5, and/or C3. The deduced protein product of *orf*14 (nucleotides 67334-68251 of SEQ ID NO:1), Orf 14 (SEQ ID NO:22) shows strong similarities to GI:3293544, a hypothetic protein with no proposed function from *Streptomyces coelicolor*, and also to GI:2654559, the human embrionic lung protein. It is also more distantly related to cation efflux system proteins like GI:2623026 from *Methanobacterium thermoautotrophicum*, so it might also take part in the export of epothilones from the producing cells. The remaining ORFs (*orf*6-*orf*13 and *orf*15) show no homologies to entries in the sequence databanks.

Example 13: Recombinant Expression of Epothilone Biosynthesis Genes

Epothilone synthase genes according to the present invention are expressed in heterologous organisms for the purposes of epothilone production at greater quantities than can be accomplished by fermentation of *Sorangium cellulosum*. A preferable host for heterologous expression is *Streptomyces*, e.g. *Streptomyces coelicolor*, which natively produces the polyketide actinorhodin. Techniques for recombinant PKS gene expression in this host are described in McDaniel *et al.*, *Science* 262: 1546-1550 (1993) and Kao *et al.*, *Science* 265: 509-512 (1994). See also, Holmes *et al.*, *EMBO Journal* 12(8): 3183-3191 (1993) and Bibb *et al.*, *Gene* 38: 215-226 (1985), as well as U.S. Patent Nos. 5,521,077, 5,672,491, and 5,712,146, which are incorporated herein by reference.

According to one method, the heterologous host strain is engineered to contain a chromosomal deletion of the actinorhodin (*act*) gene cluster. Expression plasmids containing the epothilone synthase genes of the invention are constructed by transferring DNA from a temperature-sensitive donor plasmid to a recipient shuttle vector in *E. coli* (McDaniel *et al.* (1993) and Kao *et al.* (1994)), such that the synthase genes are built-up by homologous recombination within the vector. Alternatively, the epothilone synthase gene cluster is introduced into the vector by restriction fragment ligation. Following selection, e.g. as described in Kao *et al.* (1994), DNA from the vector is introduced into the *act*-minus *Streptomyces coelicolor* strain according to protocols set forth in Hopwood *et al.*, *Genetic Manipulation of* Streptomyces. *A Laboratory Manual* (John Innes Foundation, Norwich, United Kingdom, 1985), incorporated herein by reference. The recombinant *Streptomyces* strain is grown on R2YE medium (Hopwood *et al.* (1985)) and produces epothilones. Alternatively, the epothilone synthase genes according to the present invention are expressed in other host organisms such as pseudomonads, *Bacillus*, yeast, insect cells and/or *E. coli*. PKS and NRPS genes are preferably expressed in *E. coli* using the pT7-7 vector, which uses the T7 promoter. *See*, Tabor *et al.*, *Proc. Natl. Acad. Sci. USA* 82: 1074-1078 (1985). In another embodiment, the expression vectors pKK223-3 and pKK223-2 are used to express PKS and NRPS genes in *E. coli*, either in transcriptional or translational fusion, behind the *tac or trc* promoter. Expression of PKS and NRPS genes in heterologous hosts, which do not naturally have the phosphopantetheinyl (P-pant) transferases needed for post-translational modification of PKS enzymes, requires the coexpression in the host of a P-pant transferase, as described by Kealey *et al.*, *Proc. Natl. Acad. Sci. USA* 95: 505-509 (1998).

Example 14: Isolation of Epothilones from Producing Strains

Examples of cultivation, fermentation, and extraction procedures for polyketide isolation, which are useful for extracting epothilones from both native and recombinant hosts according to the present invention, are given in WO 93/10121, incorporated herein by reference, in Example 57 of U.S. Patent No. 5,639,949, in Gerth *et al.*, *J. Antibiotics* 49: 560-563 (1996), and in Swiss patent application no. 396/98, filed February 19, 1998, and U.S. patent application no. 09/248,910 (that discloses also preferred mutant strains of Sorangium cellulosum), both of which are incorporated herein by reference. The following are procedures that are useful for isolating epothilones from cultured *Sorangium cellulosum* strains such as So ce90, and may also be used for the isolation of epothilone from recombinant hosts.

A: Cultivation of epothilone-producing strains:

Strain: *Sorangium cellulosum* Soce-90 or a recombinant host strain according to the present invention.

Preservation of the strain: In liquid N_2.

Media: Precultures and intermediate cultures: G52
Main culture: 1B12

G52 Medium:

yeast extract, low in salt (BioSpringer, Maison Alfort, France)	2 g/l
$MgSO_4$ (7 H_2O)	1 g/l
$CaCl_2$ (2 H_2O)	1 g/l
soya meal defatted Soyamine 50T (Lucas Meyer, Hamburg, Germany)	2 g/l
potato starch Noredux A-150 (Blattmann, Waedenswil, Switzerland)	8 g/l
glucose anhydrous	2 g/l
EDTA-Fe(III)-Na salt (8 g/l)	1 ml/l

pH 7.4, corrected with KOH
Sterilisation: 20 mins. 120 °C

1B12 Medium:

potato starch Noredux A-150 (Blattmann, Waedenswil, Switzerland)	20 g/l
soya meal defatted Soyamine 50T (Lucas Meyer, Hamburg, Germany)	11 g/l
EDTA-Fe(III)-Na salt	8 mg/l

pH 7.8, corrected with KOH
Sterilisation: 20 mins. 120 °C

Addition of cyclodextrins and cyclodextrin derivatives:

Cyclodextrins (Fluka, Buchs, Switzerland, or Wacker Chemie, Munich, Germany) in different concentrations are sterilised separately and added to the 1B12 medium prior to seeding.

Cultivation: 1 ml of the suspension of *Sorangium cellulosum* Soce-90 from a liquid N_2 ampoule is transferred to 10 ml of G52 medium (in a 50 ml Erlenmeyer flask) and incubated for 3 days at 180 rpm in an agitator at 30°C, 25 mm displacement. 5 ml of this culture is added to 45 ml of G52 medium (in a 200 ml Erlenmeyer flask) and incubated for 3 days at 180 rpm in an agitator at 30°C, 25 mm displacement. 50 ml of this culture is then added to 450 ml of G52 medium (in a 2 litre Erlenmeyer flask) and incubated for 3 days at 180 rpm in an agitator at 30°C, 50 mm displacement.

Maintenance culture: The culture is overseeded every 3-4 days, by adding 50 ml of culture to 450 ml of G52 medium (in a 2 litre Erlenmeyer flask). All experiments and fermentations are carried out by starting with this maintenance culture.

Tests in a flask:

(I) Preculture in an agitating flask:

Starting with the 500 ml of maintenance culture, 1 x 450 ml of G52 medium are seeded with 50 ml of the maintenance culture and incubated for 4 days at 180 rpm in an agitator at 30°C, 50 mm displacement.

(ii) Main culture in the agitating flask:

40 ml of 1B12 medium plus 5 g/l 4-morpholine-propane-sulfonic acid (= MOPS) powder (in a 200 ml Erlenmeyer flask) are mixed with 5 ml of a 10x concentrated cyclodextrin solution, seeded with 10 ml of preculture and incubated for 5 days at 180 rpm in an agitator at 30°C, 50 mm displacement.

Fermentation: Fermentations are carried out on a scale of 10 litres, 100 litres and 500 litres. 20 litre and 100 litre fermentations serve as an intermediate culture step. Whereas the pre-cultures and intermediate cultures are seeded as the maintenance culture 10% (v/v), the main cultures are seeded with 20% (v/v) of the intermediate culture. Important: In contrast to the agitating cultures, the ingredients of the media for the fermentation are calculated on the final culture volume including the inoculum. If, for example, 18 litres of medium + 2 litres of inoculum are combined, then substances for 20 litres are weighed in, but are only mixed with 18 litres.

Preculture in an agitating flask:

Starting with the 500 ml maintenance culture, 4 x 450 ml of G52 medium (in a 2 litre Erlenmeyer flask) are each seeded with 50 ml thereof, and incubated for 4 days at 180 rpm in an agitator at 30°C, 50 mm displacement.

Intermediate culture, 20 litres or 100 litres:

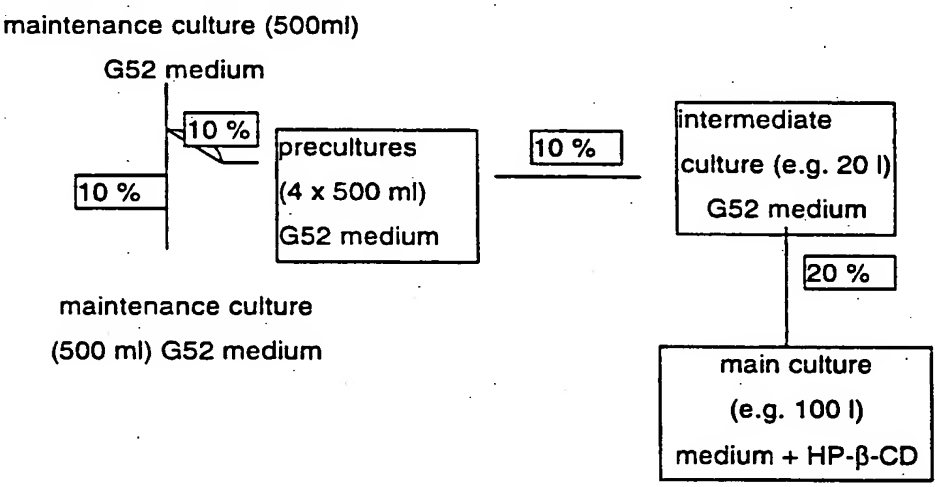
20 litres: 18 litres of G52 medium in a fermenter having a total volume of 30 litres are seeded with 2 litres of the preculture. Cultivation lasts for 3-4 days, and the conditions are: 30°C, 250 rpm, 0.5 litres of air per litre liquid per min, 0.5 bars excess pressure, no pH control.

100 litres: 90 litres of G52 medium in a fermenter having a total volume of 150 litres are seeded with 10 litres of the 20 litre intermediate culture. Cultivation lasts for 3-4 days, and the conditions are: 30°C, 150 rpm, 0.5 litres of air per litre liquid per min, 0.5 bars excess pressure, no pH control.

Main culture, 10 litres, 100 litres or 500 litres:

10 litres: The media substances for 10 litres of 1B12 medium are sterilised in 7 litres of water, then 1 litre of a sterile 10% 2-(hydroxypropyl) -β-cyclodextrin solution are added, and seeded with 2 litres of a 20 litre intermediate culture. The duration of the main culture is 6-7 days, and the conditions are: 30°C, 250 rpm, 0.5 litres of air per litre of liquid per min, 0.5 bars excess pressure, pH control with H_2SO_4/KOH to pH 7.6 +/- 0.5 (i.e. no control between pH 7.1 and 8.1).

100 litres: The media substances for 100 litres of 1B12 medium are sterilised in 70 litres of water, then 10 litres of a sterile 10% 2-(hydroxypropyl) -β-cyclodextrin solution are added, and seeded with 20 litres of a 20 litre intermediate culture. The duration of the main culture is 6-7 days, and the conditions are: 30°C, 200 rpm, 0.5 litres air per litre liquid per min., 0.5 bars excess pressure, pH control with H_2SO_4/KOH to pH 7.6 +/- 0.5. The chain of seeding for a 100 litre fermentation is shown schematically as follows:



500 litres: The media substances for 500 litres of 1B12 medium are sterilised in 350 litres of water, then 50 litres of a sterile 10% 2-(hydroxypropyl) -β-cyclodextrin solution are added, and seeded with 100 litres of a 100 litre intermediate culture. The duration of the main culture is 6-7 days, and the conditions are: 30°C, 120 rpm, 0.5 litres air per litre liquid per min., 0.5 bars excess pressure, pH control with H_2SO_4/KOH to pH 7.6 +/- 0.5.

Product analysis:

Preparation of the sample:

50 ml samples are mixed with 2 ml of polystyrene resin Amberlite XAD16 (Rohm + Haas, Frankfurt, Germany) and shaken at 180 rpm for one hour at 30°C. The resin is subsequently filtered using a 150 µm nylon sieve, washed with a little water and then added together with the filter to a 15 ml Nunc tube.

Elution of the product from the resin:

10 ml of isopropanol (>99%) are added to the tube with the filter and the resin. Afterwards, the sealed tube is shaken for 30 minutes at room temperature on a Rota-Mixer (Labinco BV, Netherlands). Then, 2 ml of the liquid are centrifuged off and the supernatant is added using a pipette to HPLC tubes.

HPLC analysis:

Column:	Waters-Symetry C18, 100 x 4 mm, 3.5 µm WAT066220 + preliminary column 3.9 x 20 mm WAT054225
Solvents:	A: 0.02 % phosphoric acid B: Acetonitrile (HPLC-Quality)
Gradient:	41% B from 0 to 7 min. 100% B from 7.2 to 7.8 min. 41% B from 8 to 12 min.
Oven temp.:	30°C
Detection:	250 nm, UV-DAD detection
Injection vol.:	10 µl
Retention time:	Epo A: 4.30 min Epo B: 5.38 min

B: Effect of the addition of cyclodextrin and cyclodextrin derivatives to the epothilone concentrations attained.

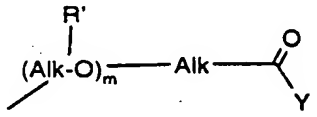
Cyclodextrins are cyclic (α-1,4)-linked oligosaccharides of α-D-glucopyranose with a relatively hydrophobic central cavity and a hydrophilic external surface area.

The following are distinguished in particular (the figures in parenthesis give the number of glucose units per molecule): α-cyclodextrin (6), β-cyclodextrin (7), γ- cyclodextrin (8), δ-cyclodextrin (9), ε- cyclodextrin (10), ζ-cyclodextrin (11), η-cyclodextrin (12), and θ–cyclodextrin (13). Especially preferred are δ-cyclodextrin and in particular α-cyclodextrin, β-cyclodextrin or γ-cyclodextrin, or mixtures thereof.

Cyclodextrin derivatives are primarily derivatives of the above-mentioned cyclodextrins, especially of α-cyclodextrin, β-cyclodextrin or γ-cyclodextrin, primarily those in which one or more up to all of the hydroxy groups (3 per glucose radical) are etherified or esterified. Ethers are primarily alkyl ethers, especially lower alkyl, such as methyl or ethyl ether, also propyl or butyl ether; the aryl-hydroxyalkyl ethers, such as phenyl-hydroxy-lower-alkyl, especially phenyl-hydroxyethyl ether; the hydroxyalkyl ethers, in particular hydroxy-lower-alkyl ethers, especially 2-hydroxyethyl, hydroxypropyl such as 2-hydroxypropyl or hydroxybutyl such as 2-hydroxybutyl ether; the carboxyalkyl ethers, in particular carboxy-lower-alkyl ethers, especially carboxymethyl or carboxyethyl ether; derivatised carboxyalkyl ethers, in particular derivatised carboxy-lower-alkyl ether in which the derivatised carboxy is etherified or amidated carboxy (primarily aminocarbonyl, mono- or di-lower-alkyl-aminocarbonyl, morpholino-, piperidino-, pyrrolidino- or piperazino-carbonyl, or alkyloxycarbonyl), in particular lower alkoxycarbonyl-lower-alkyl ether, for example methyloxycarbonylpropyl ether or ethyloxycarbonylpropyl ether; the sulfoalkyl ethers, in particular sulfo-lower-alkyl ethers, especially sulfobutyl ether; cyclodextrins in which one or more OH groups are etherified with a radical of formula

$$-O-[alk-O-]_n-H$$

wherein alk is alkyl, especially lower alkyl, and n is a whole number from 2 to 12, especially 2 to 5, in particular 2 or 3; cyclodextrins in which one or more OH groups are etherified with a radical of formula



wherein R' is hydrogen, hydroxy, $-O-(alk-O)_z-H$, $-O-(alk(-R)-O-)_p-H$ or $-O-(alk(-R)-O-)_q-alk-CO-Y$; alk in all cases is alkyl, especially lower alkyl; m, n, p, q and z are a whole number from 1 to 12, preferably 1 to 5, in particular 1 to 3; and Y is OR_1 or NR_2R_3, wherein R_1, R_2 and R_3 independently of one another, are hydrogen or lower alkyl, or R_2 and R_3 combined together with the linking nitrogen signify morpholino, piperidino, pyrrolidino or piperazino;

or branched cyclodextrins, in which etherifications or acetals with other sugar molecules are present, especially glucosyl-, diglucosyl- (G_2-β-cyclodextrin), maltosyl- or dimaltosyl-cyclodextrin, or N-acetylglucosaminyl-, glucosaminyl-, N-acetylgalactosaminyl- or galactosaminyl-cyclodextrin.

Esters are primarily alkanoyl esters, in particular lower alkanoyl esters, such as acetyl esters of cyclodextrins.

It is also possible to have cyclodextrins in which two or more different said ether and ester groups are present at the same time.

Mixtures of two or more of the said cyclodextrins and/or cyclodextrin derivatives may also exist.

Preference is given in particular to α-, β- or γ-cyclodextrins or the lower alkyl ethers thereof, such as methyl-β-cyclodextrin or in particular 2,6-di-O-methyl-β-cyclodextrin, or in particular the hydroxy lower alkyl ethers thereof, such as 2-hydroxypropyl-α–, 2-hydroxypropyl-β- or 2-hydroxypropyl-γ-cyclodextrin.

The cyclodextrins or cyclodextrin derivatives are added to the culture medium preferably in a concentration of 0.02 to 10, preferably 0.05 to 5, especially 0.1 to 4, for example 0.1 to 2 percent by weight (w/v).

Cyclodextrins or cyclodextrin derivatives are known or may be produced by known processes (see for example US 3,459,731; US 4,383,992; US 4,535,152; US 4,659,696; EP 0 094 157; EP 0 149 197; EP 0 197 571; EP 0 300 526; EP 0 320 032; EP 0 499 322; EP 0 503 710; EP 0 818 469; WO 90/12035; WO 91/11200; WO 93/19061; WO 95/08993; WO 96/14090; GB 2,189,245; DE 3,118,218; DE 3,317,064 and the references mentioned therein, which also refer to the synthesis of cyclodextrins or cyclodextrin derivatives, or also: T. Loftsson and M.E. Brewster (1996): Pharmaceutical Applications of Cyclodextrins: Drug Solubilization and Stabilisation: Journal of Pharmaceutical Science 85 (10):1017-1025; R.A. Rajewski and V.J. Stella(1996): Pharmaceutical Applications of Cyclodextrins: In Vivo Drug Delivery: Journal of Pharmaceutical Science 85 (11): 1142-1169).

All the cyclodextrin derivatives tested here are obtainable from the company Fluka, Buchs, CH. The tests are carried out in 200 ml agitating flasks with 50 ml culture volume. As controls, flasks with adsorber resin Amberlite XAD-16 (Rohm & Haas, Frankfurt, Germany) and without any adsorber addition are used. After incubation for 5 days, the following epothilone titres can be determined by HPLC:

Table 2:

Addition	order No.	Conc [%w/v][1]	Epo A [mg/l]	Epo B [mg/l]
Amberlite XAD-16 (v/v)		2.0 (%v/v)	9.2	3.8

Addition	order No.	Conc [%w/v][1]	Epo A [mg/l]	Epo B [mg/l]
2-hydroxypropyl-β-cyclodextrin	56332	0.1	2.7	1.7
2-hydroxypropyl-β-cyclodextrin	"	0.5	4.7	3.3
2-hydroxypropyl-β-cyclodextrin	"	1.0	4.7	3.4
2-hydroxypropyl-β-cyclodextrin	"	2.0	4.7	4.1
2-hydroxypropyl-β-cyclodextrin	"	5.0	1.7	0.5
2-hydroxypropyl- α-cyclodextrin	56330	0.5	1.2	1.2
2-hydroxypropyl- α-cyclodextrin	"	1.0	1.2	1.2
2-hydroxypropyl- α-cyclodextrin	"	5.0	2.5	2.3
β-cyclodextrin	28707	0.1	1.6	1.3
β-cyclodextrin	"	0.5	3.6	2.5
β-cyclodextrin	"	1.0	4.8	3.7
β-cyclodextrin	"	2.0	4.8	2.9
β-cyclodextrin	"	5.0	1.1	0.4
methyl-β-cyclodextrin	66292	0.5	0.8	<0.3
methyl-β-cyclodextrin	"	1.0	<0.3	<0.3
methyl-β-cyclodextrin	"	2.0	<0.3	<0.3
2,6 di-o-methyl-β-cyclodextrin	39915	1.0	<0.3	<0.3
2-hydroxypropyl-γ-cyclodextrin	56334	0.1	0.3	<0.3
2-hydroxypropyl-γ-cyclodextrin	"	0.5	0.9	0.8
2-hydroxypropyl-γ-cyclodextrin	"	1.0	1.1	0.7
2-hydroxypropyl-γ-cyclodextrin	"	2.0	2.6	0.7
2-hydroxypropyl-γ-cyclodextrin	"	5.0	5.0	1.1
no addition			**0.5**	**0.5**

[1]) Apart from Amberlite (%v/v), all percentages are by weight (%w/v).

Few of the cyclodextrins tested (2,6-di-o-methyl-β-cyclodextrin, methyl-β-cyclodextrin) display no effect or a negative effect on epothilone production at the concentrations used. 1-2% 2-hydroxy-propyl-β-cyclodextrin and β-cyclodextrin increase epothilone production in the examples by 6 to 8 times compared with production using no cyclodextrins.

C: 10 litre fermentation with 1% 2-(hydroxypropyl)-β-cyclodextrin):

Fermentation is carried out in a 15 litre glass fermenter. The medium contains 10 g/l of 2-(hydroxypropyl)-β-cyclodextrin from Wacker Chemie, Munich, Germany. The progress of fermentation is illustrated in Table 3. Fermentation is ended after 6 days and working up takes place.

Table 3: Progress of a 10 litre fermentation

duration of culture [d]	Epothilone A [mg/l]	Epothilone B [mg/l]
0	0	0
1	0	0
2	0.5	0.3
3	1.8	2.5
4	3.0	5.1
5	3.7	5.9
6	3.6	5.7

D: 100 litre fermentation with 1% 2-(hydroxypropyl)-β-cyclodextrin):

Fermentation is carried out in a 150 litre fermenter. The medium contains 10 g/l of 2-(Hydroxypropyl)-β-cyclodextrin. The progress of fermentation is illustrated in Table 4. The fermentation is harvested after 7 days and worked up.

Table 4: Progress of a 100 litre fermentation

duration of culture [d]	Epothilone A [mg/l]	Epothilone B [mg/l]
0	0	0
1	0	0
2	0.3	0

3	0.9	1.1
4	1.5	2.3
5	1.6	3.3
6	1.8	3.7
7	1.8	3.5

E: 500 litre fermentation with 1% 2-(hydroxypropyl)-β-cyclodextrin):

Fermentation is carried out in a 750 litre fermenter. The medium contains 10 g/l of 2-(Hydroxypropyl)-β-cyclodextrin. The progress of fermentation is illustrated in Table 5. The fermentation is harvested after 7 days and worked up.

Table 5: Progress of a 500 litre fermentation

duration of culture [d]	Epothilone A [mg/l]	Epothilone B [mg/l]
0	0	0
1	0	0
2	0	0
3	0.6	0.6
4	1.7	2.2
5	3.1	4.5
6	3.1	5.1

F: Comparison example 10 litre fermentation without adding an adsorber:

Fermentation is carried out in a 15 litre glass fermenter. The medium does not contain any cyclodextrin or other adsorber. The progress of fermentation is illustrated in Table 6. The fermentation is not harvested and worked up.

Table 6: Progress of a 10 litre fermentation without adsorber.

duration of culture [d]	Epothilone A [mg/l]	Epothilone B [mg/l]
0	0	0
1	0	0
2	0	0
3	0	0
4	0.7	0.7
5	0.7	1.0
6	0.8	1.3

G: Working up of the epothilones: Isolation from a 500 litre main culture:

The volume of harvest from the 500 litre main culture of example 2D is 450 litres and is separated using a Westfalia clarifying separator Type SA-20-06 (rpm = 6500) into the liquid phase (centrifugate + rinsing water = 650 litres) and solid phase (cells = ca. 15 kg). The main part of the epothilones are found in the centrifugate, The centrifuged cell pulp contains < 15% of the determined epothilone portion and is not further processed. The 650 litre centrifugate is then placed in a 4000 litre stirring vessel, mixed with 10 litres of Amberlite XAD-16 (centrifugate:resin volume = 65:1) and stirred. After a period of contact of ca. 2 hours, the resin is centrifuged away in a Heine overflow centrifuge (basket content 40 litres; rpm = 2800). The resin is discharged from the centrifuge and washed with 10-15 litres of deionised water. Desorption is effected by stirring the resin twice, each time in portions with 30 litres of isopropanol in 30 litre glass stirring vessels for 30 minutes. Separation of the isopropanol phase from the resin takes place using a suction filter. The isopropanol is then removed from the combined isopropanol phases by adding 15-20 litres of water in a vacuum-operated circulating evaporator (Schmid-Verdampfer) and the resulting water phase of ca. 10 litres is extracted 3x each time with 10 litres of ethyl acetate. Extraction is effected in 30 litre glass stirring vessels. The ethyl acetate extract is concentrated to 3-5 litres in a vacuum-operated circulating evaporator (Schmid-Verdampfer) and afterwards concentrated to dryness in a rotary evaporator (Büchi type) under vacuum. The result is an ethyl acetate extract of 50.2 g. The ethyl acetate extract is dissolved in

500 ml of methanol, the insoluble portions filtered off using a folded filter, and the solution added to a 10 kg Sephadex LH 20 column (Pharmacia, Uppsala, Sweden) (column diameter 20 cm, filling level ca. 1.2 m). Elution is effected with methanol as eluant. Epothilone A and B is present predominantly in fractions 21-23 (at a fraction size of 1 litre). These fractions are concentrated to dryness in a vacuum on a rotary evaporator (total weight 9.0 g). These Sephadex peak fractions (9.0 g) are thereafter dissolved in 92 ml of acetonitrile:-water:-methylene chloride = 50:40:2, the solution filtered through a folded filter and added to a RP column (equipment Prepbar 200, Merck; 2. 0 kg LiChrospher RP-18 Merck, grain size 12µm, column diameter 10 cm, filling level 42 cm; Merck, Darmstadt, Germany). Elution is effected with acetonitrile:water = 3:7 (flow rate = 500 ml/min.; retention time of epothilone A = ca. 51-59 mins.; retention time of epothilone B = ca. 60-69 mins.). Fractionation is monitored with a UV detector at 250 nm. The fractions are concentrated to dryness under vacuum on a Büchi-Rotavapor rotary evaporator. The weight of the epothilone A peak fraction is 700 mg, and according to HPLC (external standard) it has a content of 75.1%. That of the epothilone B peak fraction is 1980 mg, and the content according to HPLC (external standard) is 86.6%. Finally, the epothilone A fraction (700 mg) is crystallised from 5 ml of ethyl acetate:toluene = 2:3, and yields 170 mg of epothilone A pure crystallisate [content according to HLPC (% of area) = 94.3%]. Crystallisation of the epothilone B fraction (1980 mg) is effected from 18 ml of methanol and yields 1440 mg of epothilone B pure crystallisate [content according to HPLC (% of area) = 99.2%]. m.p. (Epothilone B): e.g. 124-125 °C; ^{1}H-NMR data for Epothilone B:
500 MHz-NMR, solvent: DMSO-d6. Chemical displacement δ in ppm relative to TMS. s = singlet; d = doublet; m = multiplet

δ (Multiplicity)	Integral (number of H)
7.34 (s)	1
6.50 (s)	1
5.28 (d)	1
5.08 (d)	1
4.46 (d)	1
4.08 (m)	1

3.47 (m)	1
3.11 (m)	1
2.83 (dd)	1
2.64 (s)	3
2.36 (m)	2
2.09 (s)	3
2.04 (m)	1
1.83 (m)	1
1.61 (m)	1
1.47 - 1.24 (m)	4
1.18 (s)	6
1.13 (m)	2
1.06 (d)	3
0.89 (d + s, overlapping)	6
	$\Sigma = 41$

Example 15: Medical Uses of Recombinantly Produced Epothilones

Pharmaceutical preparations or compositions comprising epothilones are used for example in the treatment of cancerous diseases, such as various human solid tumors. Such anticancer formulations comprise, for example, an active amount of an epothilone together with one or more organic or inorganic, liquid or solid, pharmaceutically suitable carrier materials. Such formulations are delivered, for example, enterally, nasally, rectally, orally, or parenterally, particularly intramuscularly or intravenously. The dosage of the active ingredient is dependent upon the weight, age, and physical and pharmacokinetical condition of the patient and is further dependent upon the method of delivery. Because epothilones mimic the biological effects of taxol, epothilones may be substituted for taxol in compositions and methods utilizing taxol in the treatment of cancer. *See*, for example, U.S.

Patent Nos. 5,496,804, 5,565,478, and 5,641,803, all of which are incorporated herein by reference.

For example, for treatments, epothilone B is supplied in individual 2 ml glass vials formulated as 1 mg/1 ml of clear, colorless intravenous concentrate. The substance is formulated in polyethylene glycol 300 (PEG 300) and diluted with 50 or 100 ml 0.9% Sodium Chloride Injection, USP, to achieve the desired final concentration of the drug for infusion. It is administered as a single 30-minute intravenous infusion every 21 days (treatment three-weekly) for six cycles, or as a single 30-minute intravenous infusion every 7 days (weekly treatment).

Preferably, for weekly treatment, the dose is between about 0.1 and about 6, preferably about 0.1 and about 5 mg/m^2, more preferably about 0.1 and about 3 mg/m^2, even more preferably 0.1 and 1.7 mg/m^2, most preferably about 0.3 and about 1 mg/m^2; for three-weekly treatment (treatment every three weeks or every third week) the dose is between about 0.3 and about 18 mg/m^2, preferably about 0.3 and about 15 mg/m^2, more preferably about 0.3 and about 12 mg/m^2, even more preferably about 0.3 and about 7.5 mg/m^2, still more preferably about 0.3 and about 5 mg/m^2, most preferably about 1.0 and about 3.0 mg/m^2. This dose is preferably administered to the human by intravenous (i.v.) administration during 2 to 180 min, preferably 2 to 120 min, more preferably during about 5 to about 30 min, most preferably during about 10 to about 30 min, e.g. during about 30 min.

While the present invention has been described with reference to specific embodiments thereof, it will be appreciated that numerous variations, modifications, and embodiments are possible, and accordingly, all such variations, modifications and embodiments are to be regarded as being within the spirit and scope of the present invention.

BUDAPEST TREATY ON THE INTERNATIONAL
RECOGNITION OF THE DEPOSIT OF MICROORGANISMS
FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novartis AG
Novartis Corporation
Patent and Trademark Dept.
3054 Cornwallis Rd.
Research Triangle Park, NC 27709

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT
issued pursuant to Rule 7.1 by the
INTERNATIONAL DEPOSITARY AUTHORITY
identified at the bottom of this page

NAME AND ADDRESS
OF DEPOSITOR

I. IDENTIFICATION OF THE MICROORGANISM

Identification reference given by the DEPOSITOR:	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY:
Escherichia coli DH10B [pEP015]	NRRL B-30033

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

☐ a scientific description

☒ a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on June 11, 1998(date of the original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I. above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: 7-21-98

[1] Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSE OF PATENT PROCEDURES

INTERNATIONAL FORM

TO
Novatis AG
c/o Novartis Agricultural Biotechnology Research, Inc.
Patent & Trademark Department
3054 Cornwallis Road
Research Triangle Park, NC 27709
NAME AND ADDRESS OF DEPOSITOR

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT issued pursuant to Rule 7.1 by the INTERNATIONAL DEPOSITARY AUTHORITY identified at the bottom of this page

I. IDENTIFICATION OF THE MICROORGANISM	
Identification reference given by the DEPOSITOR: Escherichia coli DH10B [pEPO32]	Accession number given by the INTERNATIONAL DEPOSITARY AUTHORITY: NRRL B-30119

II. SCIENTIFIC DESCRIPTION AND/OR PROPOSED TAXONOMIC DESIGNATION

The microorganism identified under I. above was accompanied by:

☐ a scientific description

☒ a proposed taxonomic designation

(Mark with a cross where applicable)

III. RECEIPT AND ACCEPTANCE

This International Depositary Authority accepts the microorganism identified under I. above, which was received by it on April 16, 1999 (date of the original deposit)[1]

IV. RECEIPT OF REQUEST FOR CONVERSION

The microorganism identified under I. above was received by this International Depositary Authority on (date of the original deposit) and a request to convert the original deposit to a deposit under the Budapest Treaty was received by it on (date of receipt of request for conversion).

V. INTERNATIONAL DEPOSITARY AUTHORITY

Name: Agricultural Research Culture Collection (NRRL) International Depositary Authority Address: 1815 N. University Street Peoria, Illinois 61604 U.S.A.	Signature(s) of person(s) having the power to represent the International Depositary Authority or of authorized official(s): Date: 5-24-99

[1] Where Rule 6.4(d) applies, such date is the date on which the status of international depositary authority was acquired.

What is claimed is:

1. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes at least one polypeptide involved in the biosynthesis of epothilone.

2. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence is isolated from a myxobacterium.

3. An isolated nucleic acid molecule according to claim 2, wherein said myxobacterium is *Sorangium cellulosum*.

4. A chimeric gene comprising a heterologous promoter sequence operatively linked to a nucleic acid molecule according to claim 1.

5. A recombinant vector comprising a chimeric gene according to claim 4.

6. A recombinant host cell comprising a chimeric gene according to claim 4.

7. The recombinant host cell of claim 6, which is a bacteria.

8. The recombinant host cell of claim 7, which is an Actinomycete.

9. The recombinant host cell of claim 8, which is *Streptomyces*.

10. A Bac clone comprising a nucleic acid molecule according to claim 1.

11. The Bac clone of claim 10, which is pEPO15.

12. An isolated nucleic acid molecule according to claim 1, wherein said polypeptide comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: SEQ ID NO:2, amino acids 11-437 of SEQ ID NO:2, amino acids 543-864 of SEQ ID NO:2, amino acids 974-1273 of SEQ ID NO:2, amino acids 1314-1385 of SEQ ID NO:2, SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids

118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, amino acids 1344-1351 of SEQ ID NO:3, SEQ ID NO:4, amino acids 7-432 of SEQ ID NO:4, amino acids 539-859 of SEQ ID NO:4, amino acids 869-1037 of SEQ ID NO:4, amino acids 1439-1684 of SEQ ID NO:4, amino acids 1722-1792 of SEQ ID NO:4, SEQ ID NO:5, amino acids 39-457 of SEQ ID NO:5, amino acids 563-884 of SEQ ID NO:5, amino acids 1147-1399 of SEQ ID NO:5, amino acids 1434-1506 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 3886-4048 of SEQ ID NO:5, amino acids 4433-4719 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, SEQ ID NO:6, amino acids 35-454 of SEQ ID NO:6, amino acids 561-881 of SEQ ID NO:6, amino acids 1143-1393 of SEQ ID NO:6, amino acids 1430-1503 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, amino acids 2053-2373 of SEQ ID NO:6, amino acids 2383-2551 of SEQ ID NO:6, amino acids 2671-3045 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, SEQ ID NO:7, amino acids 32-450 of SEQ ID NO:7, amino acids 556-877 of SEQ ID NO:7, amino acids 887-1051 of SEQ ID NO:7, amino acids 1478-1790 of SEQ ID NO:7, amino acids 1810-2055 of SEQ ID NO:7, amino acids 2093-2164 of SEQ ID NO:7, amino acids 2165-2439 of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:22.

13. An isolated nucleic acid molecule according to claim 12, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:2, amino acids 11-437 of SEQ ID NO:2, amino acids 543-864 of SEQ ID NO:2, amino acids 974-1273 of SEQ ID NO:2, amino acids 1314-1385 of SEQ ID NO:2, SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino

acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, amino acids 1344-1351 of SEQ ID NO:3, SEQ ID NO:4, amino acids 7-432 of SEQ ID NO:4, amino acids 539-859 of SEQ ID NO:4, amino acids 869-1037 of SEQ ID NO:4, amino acids 1439-1684 of SEQ ID NO:4, amino acids 1722-1792 of SEQ ID NO:4, SEQ ID NO:5, amino acids 39-457 of SEQ ID NO:5, amino acids 563-884 of SEQ ID NO:5, amino acids 1147-1399 of SEQ ID NO:5, amino acids 1434-1506 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 3886-4048 of SEQ ID NO:5, amino acids 4433-4719 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, SEQ ID NO:6, amino acids 35-454 of SEQ ID NO:6, amino acids 561-881 of SEQ ID NO:6, amino acids 1143-1393 of SEQ ID NO:6, amino acids 1430-1503 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, amino acids 2053-2373 of SEQ ID NO:6, amino acids 2383-2551 of SEQ ID NO:6, amino acids 2671-3045 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, SEQ ID NO:7, amino acids 32-450 of SEQ ID NO:7, amino acids 556-877 of SEQ ID NO:7, amino acids 887-1051 of SEQ ID NO:7, amino acids 1478-1790 of SEQ ID NO:7, amino acids 1810-2055 of SEQ ID NO:7, amino acids 2093-2164 of SEQ ID NO:7, amino acids 2165-2439 of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:22.

14. An isolated nucleic acid molecule according to claim 12, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: the complement of nucleotides 1900-3171 of SEQ ID NO:1, nucleotides 3415-5556 of SEQ ID NO:1, nucleotides 7610-11875 of SEQ ID NO:1, nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 10529-11428 of SEQ

ID NO:1, nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, nucleotides 15901-15924 of SEQ ID NO:1, nucleotides 16251-21749 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 21746-43519 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 43524-54920 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, nucleotides 51534-52657 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, nucleotides 54935-62254 of SEQ ID NO:1, nucleotides 55028-56284 of SEQ ID NO:1, nucleotides 56600-57565 of SEQ ID NO:1, nucleotides 57593-58087 of SEQ ID NO:1, nucleotides 59366-60304 of SEQ ID NO:1, nucleotides 60362-61099 of SEQ ID NO:1, nucleotides 61211-61426 of SEQ ID NO:1, nucleotides 61427-62254 of SEQ ID NO:1, nucleotides 62369-63628 of SEQ ID NO:1, nucleotides 67334-68251 of SEQ ID NO:1, and nucleotides 1-68750 SEQ ID NO:1.

15. A nucleic acid molecule according to claim 12, wherein said nucleotide sequence is selected from the group consisting of: the complement of nucleotides 1900-3171 of SEQ ID NO:1, nucleotides 3415-5556 of SEQ ID NO:1, nucleotides 7610-11875 of SEQ ID NO:1, nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, nucleotides 15901-15924 of SEQ ID NO:1, nucleotides 16251-21749 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 21746-43519 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 43524-54920 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, nucleotides 51534-52657 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID

NO:1, nucleotides 54935-62254 of SEQ ID NO:1, nucleotides 55028-56284 of SEQ ID NO:1, nucleotides 56600-57565 of SEQ ID NO:1, nucleotides 57593-58087 of SEQ ID NO:1, nucleotides 59366-60304 of SEQ ID NO:1, nucleotides 60362-61099 of SEQ ID NO:1, nucleotides 61211-61426 of SEQ ID NO:1, nucleotides 61427-62254 of SEQ ID NO:1, nucleotides 62369-63628 of SEQ ID NO:1, nucleotides 67334-68251 of SEQ ID NO:1, and nucleotides 1-68750 SEQ ID NO:1.

16. A chimeric gene comprising a heterologous promoter sequence operatively linked to a nucleic acid molecule according to claim 12.

17. A recombinant vector comprising a chimeric gene according to claim 16.

18. A recombinant host cell comprising a chimeric gene according to claim 16.

19. The recombinant host cell of claim 18, which is a bacteria.

20. The recombinant host cell of claim 19, which is an Actinomycete.

21. The recombinant host cell of claim 20, which is *Streptomyces*.

22. An isolated nucleic acid molecule according to claim 1, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: the complement of nucleotides 1900-3171 of SEQ ID NO:1, nucleotides 3415-5556 of SEQ ID NO:1, nucleotides 7610-11875 of SEQ ID NO:1, nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID

NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, nucleotides 15901-15924 of SEQ ID NO:1, nucleotides 16251-21749 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 21746-43519 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 43524-54920 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, nucleotides 51534-52657 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, nucleotides 54935-62254 of SEQ ID NO:1, nucleotides 55028-56284 of SEQ ID NO:1, nucleotides 56600-57565 of SEQ ID NO:1, nucleotides 57593-58087 of SEQ ID NO:1, nucleotides 59366-60304 of SEQ ID NO:1, nucleotides 60362-61099 of SEQ ID NO:1, nucleotides 61211-61426 of SEQ ID NO:1, nucleotides 61427-62254 of SEQ ID NO:1, nucleotides 62369-63628 of SEQ ID NO:1, nucleotides 67334-68251 of SEQ ID NO:1, and nucleotides 1-68750 SEQ ID NO:1.

23. A chimeric gene comprising a heterologous promoter sequence operatively linked to a nucleic acid molecule according to claim 22.

24. A recombinant vector comprising a chimeric gene according to claim 23.

25. A recombinant host cell comprising a chimeric gene according to claim 23.

26. The recombinant host cell of claim 25, which is a bacteria.

27. The recombinant host cell of claim 26, which is an Actinomycete.

28. The recombinant host cell of claim 27, which is *Streptomyces*.

29. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes at least one epothilone synthase domain.

30. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is a β-ketoacyl-synthase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7.

31. An isolated nucleic acid molecule according to claim 30, wherein said β-ketoacyl-synthase domain comprises an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7.

32. An isolated nucleic acid molecule according to claim 30, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, and nucleotides 55028-56284 of SEQ ID NO:1.

33. An isolated nucleic acid molecule according to claim 30, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, and nucleotides 55028-56284 of SEQ ID NO:1.

34. An isolated nucleic acid molecule according to claim 30, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 7643-8920 of SEQ ID NO:1, nucleotides 16269-17546 of SEQ ID NO:1, nucleotides 21860-23116 of SEQ ID NO:1, nucleotides 26318-27595 of SEQ ID NO:1, nucleotides 30815-32092 of SEQ ID NO:1, nucleotides 37052-38320 of SEQ ID NO:1, nucleotides 43626-44885 of SEQ ID NO:1, nucleotides 48087-49361 of SEQ ID NO:1, and nucleotides 55028-56284 of SEQ ID NO:1.

35. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is a an acyltransferase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7.

36. An isolated nucleic acid molecule according to claim 35, wherein said acyltransferase domain comprises an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7.

37. An isolated nucleic acid molecule according to claim 35, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, and nucleotides 56600-57565 of SEQ ID NO:1.

38. An isolated nucleic acid molecule according to claim 35, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, and nucleotides 56600-57565 of SEQ ID NO:1.

39. An isolated nucleic acid molecule according to claim 35, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 9236-10201 of SEQ ID NO:1, nucleotides 17865-18827 of SEQ ID NO:1, nucleotides 23431-24397 of SEQ ID NO:1, nucleotides 27911-28876 of SEQ ID NO:1, nucleotides 32408-33373 of SEQ ID NO:1, nucleotides 38636-39598 of SEQ ID NO:1, nucleotides 45204-46166 of SEQ ID NO:1, nucleotides 49680-50642 of SEQ ID NO:1, and nucleotides 56600-57565 of SEQ ID NO:1.

40. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is an enoyl reductase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7.

41. An isolated nucleic acid molecule according to claim 40, wherein said enoyl reductase domain comprises an amino acid sequence selected from the group consisting

of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7.

42. An isolated nucleic acid molecule according to claim 40, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, and nucleotides 59366-60304 of SEQ ID NO:1.

43. An isolated nucleic acid molecule according to claim 40, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, and nucleotides 59366-60304 of SEQ ID NO:1.

44. An isolated nucleic acid molecule according to claim 40, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 10529-11428 of SEQ ID NO:1, nucleotides 35042-35902 of SEQ ID NO:1, nucleotides 41369-42256 of SEQ ID NO:1, and nucleotides 59366-60304 of SEQ ID NO:1.

45. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is an acyl carrier protein domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7.

46. An isolated nucleic acid molecule according to claim 45, wherein said acyl carrier protein domain comprises an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID

NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7.

47. An isolated nucleic acid molecule according to claim 45, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, and nucleotides 61211-61426 of SEQ ID NO:1.

48. An isolated nucleic acid molecule according to claim 45, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, and nucleotides 61211-61426 of SEQ ID NO:1.

49. An isolated nucleic acid molecule according to claim 45, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 11549-11764 of SEQ ID NO:1, nucleotides 21414-21626 of SEQ ID NO:1, nucleotides 26045-26263 of SEQ ID NO:1, nucleotides 30539-30759 of SEQ ID NO:1, nucleotides 36773-36991 of SEQ ID NO:1, nucleotides 43163-43378 of SEQ ID NO:1, nucleotides 47811-48032 of SEQ ID NO:1, nucleotides 54540-54758 of SEQ ID NO:1, and nucleotides 61211-61426 of SEQ ID NO:1.

50. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is a dehydratase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of:

amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7.

51. An isolated nucleic acid molecule according to claim 50, wherein said dehydratase domain comprises an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7.

52. An isolated nucleic acid molecule according to claim 50, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, and nucleotides 57593-58087 of SEQ ID NO:1.

53. An isolated nucleic acid molecule according to claim 50, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, and nucleotides 57593-58087 of SEQ ID NO:1.

54. An isolated nucleic acid molecule according to claim 50, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 18855-19361 of SEQ ID NO:1, nucleotides 33401-33889 of SEQ ID NO:1, nucleotides 39635-40141 of SEQ ID NO:1, nucleotides 50670-51176 of SEQ ID NO:1, and nucleotides 57593-58087 of SEQ ID NO:1.

55. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is a β-ketoreductase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino

acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7.

56. An isolated nucleic acid molecule according to claim 55, wherein said β-ketoreductase domain comprises an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7.

57. An isolated nucleic acid molecule according to claim 55, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, and nucleotides 60362-61099 of SEQ ID NO:1.

58. An isolated nucleic acid molecule according to claim 55, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, and nucleotides 60362-61099 of SEQ ID NO:1.

59. An isolated nucleic acid molecule according to claim 55, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 20565-21302 of SEQ ID NO:1, nucleotides 25184-25942 of SEQ ID NO:1, nucleotides 29678-30429 of SEQ ID NO:1, nucleotides 35930-36667 of SEQ ID NO:1, nucleotides 42314-43048 of SEQ ID

NO:1, nucleotides 46950-47702 of SEQ ID NO:1, nucleotides 53697-54431 of SEQ ID NO:1, and nucleotides 60362-61099 of SEQ ID NO:1.

60. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is a methyltransferase domain comprising an amino acid sequence substantially similar to amino acids 2671-3045 of SEQ ID NO:6.

61. An isolated nucleic acid molecule according to claim 60, wherein said methyltransferase domain comprises amino acids 2671-3045 of SEQ ID NO:6.

62. An isolated nucleic acid molecule according to claim 60, wherein said nucleotide sequence is substantially similar to nucleotides 51534-52657 of SEQ ID NO:1.

63. An isolated nucleic acid molecule according to claim 60, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of nucleotides 51534-52657 of SEQ ID NO:1.

64. An isolated nucleic acid molecule according to claim 60, wherein said nucleotide sequence is nucleotides 51534-52657 of SEQ ID NO:1.

65. An isolated nucleic acid molecule according to claim 29, wherein said epothilone synthase domain is a thioesterase domain comprising an amino acid sequence substantially similar to amino acids 2165-2439 of SEQ ID NO:7.

66. An isolated nucleic acid molecule according to claim 65, wherein said thioesterase domain comprises amino acids 2165-2439 of SEQ ID NO:7.

67. An isolated nucleic acid molecule according to claim 65, wherein said nucleotide sequence is substantially similar to nucleotides 61427-62254 of SEQ ID NO:1.

68. An isolated nucleic acid molecule according to claim 65, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of nucleotides 61427-62254 of SEQ ID NO:1.

69. An isolated nucleic acid molecule according to claim 65, wherein said nucleotide sequence is nucleotides 61427-62254 of SEQ ID NO:1.

70. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a non-ribosomal peptide synthetase, wherein said non-ribosomal peptide synthetase comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, and amino acids 1344-1351 of SEQ ID NO:3.

71. An isolated nucleic acid molecule according to claim 70, wherein said non-ribosomal peptide synthetase comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:3, amino acids 72-81 of SEQ ID NO:3, amino acids 118-125 of SEQ ID NO:3, amino acids 199-212 of SEQ ID NO:3, amino acids 353-363 of SEQ ID NO:3, amino acids 549-565 of SEQ ID NO:3, amino acids 588-603 of SEQ ID NO:3, amino acids 669-684 of SEQ ID NO:3, amino acids 815-821 of SEQ ID NO:3, amino acids 868-892 of SEQ ID NO:3, amino acids 903-912 of SEQ ID NO:3, amino acids 918-940 of SEQ ID NO:3, amino acids 1268-1274 of SEQ ID NO:3, amino acids 1285-1297 of SEQ ID NO:3, amino acids 973-1256 of SEQ ID NO:3, and amino acids 1344-1351 of SEQ ID NO:3.

72. An isolated nucleic acid molecule according to claim 70, wherein said nucleotide sequence is substantially similar to a nucleotide sequence selected from the group consisting of: nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID

NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, and nucleotides 15901-15924 of SEQ ID NO:1.

73. An isolated nucleic acid molecule according to claim 70, wherein said nucleotide sequence comprises a consecutive 20 base pair nucleotide portion identical in sequence to a consecutive 20 base pair portion of a nucleotide sequence selected from the group consisting of: nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, and nucleotides 15901-15924 of SEQ ID NO:1.

74. An isolated nucleic acid molecule according to claim 70, wherein said nucleotide sequence is selected from the group consisting of: nucleotides 11872-16104 of SEQ ID NO:1, nucleotides 12085-12114 of SEQ ID NO:1, nucleotides 12223-12246 of SEQ ID NO:1, nucleotides 12466-12507 of SEQ ID NO:1, nucleotides 12928-12960 of SEQ ID NO:1, nucleotides 13516-13566 of SEQ ID NO:1, nucleotides 13633-13680 of SEQ ID NO:1, nucleotides 13876-13923 of SEQ ID NO:1, nucleotides 14313-14334 of SEQ ID NO:1, nucleotides 14473-14547 of SEQ ID NO:1, nucleotides 14578-14607 of SEQ ID NO:1, nucleotides 14623-14692 of SEQ ID NO:1, nucleotides 15673-15693 of SEQ ID NO:1, nucleotides 15724-15762 of SEQ ID NO:1, nucleotides 14788-15639 of SEQ ID NO:1, and nucleotides 15901-15924 of SEQ ID NO:1.

75. A method for heterologous expression of epothilone in a recombinant host, comprising:

(a) introducing a chimeric gene according to claim 4 into a host; and

(b) growing the host in conditions that allow biosynthesis of epothilone in the host.

76. A method for producing epothilone, comprising:

(a) expressing epothilone in a recombinant host by the method of claim 75; and

(b) extracting epothilone from the recombinant host.

77. An isolated polypeptide comprising an amino acid sequence that consists of an epothilone synthase domain.

78. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is a β-ketoacyl-synthase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7.

79. An isolated polypeptide according to claim 78, wherein said β-ketoacyl-synthase domain comprises an amino acid sequence selected from the group consisting of: amino acids 11-437 of SEQ ID NO:2, amino acids 7-432 of SEQ ID NO:4, amino acids 39-457 of SEQ ID NO:5, amino acids 1524-1950 of SEQ ID NO:5, amino acids 3024-3449 of SEQ ID NO:5, amino acids 5103-5525 of SEQ ID NO:5, amino acids 35-454 of SEQ ID NO:6, amino acids 1522-1946 of SEQ ID NO: 6, and amino acids 32-450 of SEQ ID NO:7.

80. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is an acyltransferase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7.

81. An isolated polypeptide according to claim 80, wherein said acyltransferase domain comprises an amino acid sequence selected from the group consisting of: amino

acids 543-864 of SEQ ID NO:2, amino acids 539-859 of SEQ ID NO:4, amino acids 563-884 of SEQ ID NO:5, amino acids 2056-2377 of SEQ ID NO:5, amino acids 3555-3876 of SEQ ID NO:5, amino acids 5631-5951 of SEQ ID NO:5, amino acids 561-881 of SEQ ID NO:6, amino acids 2053-2373 of SEQ ID NO:6, and amino acids 556-877 of SEQ ID NO:7.

82. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is an enoyl reductase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7.

83. An isolated polypeptide according to claim 82, wherein said enoyl reductase domain comprises an amino acid sequence selected from the group consisting of: amino acids 974-1273 of SEQ ID NO:2, amino acids 4433-4719 of SEQ ID NO:5, amino acids 6542-6837 of SEQ ID NO:5, and amino acids 1478-1790 of SEQ ID NO:7.

84. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is an acyl carrier protein domain, wherein said polypeptide comprises an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7.

85. An isolated polypeptide according to claim 84, wherein said acyl carrier protein domain comprises an amino acid sequence selected from the group consisting of: amino acids 1314-1385 of SEQ ID NO:2, amino acids 1722-1792 of SEQ ID NO:4, amino acids 1434-1506 of SEQ ID NO:5, amino acids 2932-3005 of SEQ ID NO:5, amino acids 5010-5082 of SEQ ID NO:5, amino acids 7140-7211 of SEQ ID NO:5, amino acids 1430-1503 of SEQ ID NO:6, amino acids 3673-3745 of SEQ ID NO:6, and amino acids 2093-2164 of SEQ ID NO:7.

86. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is a dehydratase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7.

87. An isolated polypeptide according to claim 86, wherein said dehydratase domain comprises an amino acid sequence selected from the group consisting of: amino acids 869-1037 of SEQ ID NO:4, amino acids 3886-4048 of SEQ ID NO:5, amino acids 5964-6132 of SEQ ID NO:5, amino acids 2383-2551 of SEQ ID NO:6, and amino acids 887-1051 of SEQ ID NO:7.

88. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is a β-ketoreductase domain comprising an amino acid sequence substantially similar to an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7.

89. An isolated polypeptide according to claim 88, wherein said β-ketoreductase domain comprises an amino acid sequence selected from the group consisting of: amino acids 1439-1684 of SEQ ID NO:4, amino acids 1147-1399 of SEQ ID NO:5, amino acids 2645-2895 of SEQ ID NO:5, amino acids 4729-4974 of SEQ ID NO:5, amino acids 6857-7101 of SEQ ID NO:5, amino acids 1143-1393 of SEQ ID NO:6, amino acids 3392-3636 of SEQ ID NO:6, and amino acids 1810-2055 of SEQ ID NO:7.

90. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is a methyltransferase domain comprising an amino acid sequence substantially similar to amino acids 2671-3045 of SEQ ID NO:6.

91. An isolated polypeptide according to claim 90, wherein said methyltransferase domain comprises amino acids 2671-3045 of SEQ ID NO:6.

92. An isolated polypeptide according to claim 77, wherein said epothilone synthase domain is a thioesterase domain comprising an amino acid sequence substantially similar to amino acids 2165-2439 of SEQ ID NO:7.

93. An isolated polypeptide according to claim 77, wherein said thioesterase domain comprises amino acids 2165-2439 of SEQ ID NO:7.

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cgtctggctc gggcaccgcc tgggaaaccc ctacctcgac ggcgcggcgt cgatcggcat 67920
cggcctcgtg ctcgccgcgg tcgcggtctt cctcgccagc cagagccgtg ggctcctcgt 67980
gggggagagc gcggacaggg agctcctcgc cgcgatccgc gcgctcgcca gcgcagatcc 68040
tggcgtgtcg gcggtggggc ggcccctgac gatgcacttc ggtccgcacg aagtcctggt 68100
cgtgctgcgc atcgagttcg acgccgcgct cacggcgtcc ggggtcgcgg aggcgatcga 68160
gcgcatcgag acccggatac ggagcgagcg acccgacgtg aagcacatct acgtcgaggc 68220
caggtcgctc caccagcgcg cgagggcgtg acgcgccgtg gagagaccgc gcgcggcctc 68280
cgccatcctc cgcggcgccc gggctcaggt ggccctcgca gcagggcgcg cctggcgggc 68340
aaaccgtgca gacgtcgtcc ttcgacgcga ggtacgctgg ttgcaagtcg tcacgccgta 68400
tcgcgaggtc cggcagcgcc ggagcccggg cgggccgggc gcacgaaggc gcggcgagcg 68460
caggcttcga gggggggcgac gtcatgagga aggccagggc gcatggggcg atgctcggcg 68520
ggcgagatga cggctggcgt cgcggcctcc ccggcgccgg cgcgcttcgc gccgcgctcc 68580
agcgcggtcg ctcgcgcgat ctcgcccggc gccggctcat cgcctccgtg tccctcgccg 68640
gcggcgccag catggcggtc gtctcgctgt tccagctcgg gatcatcgag cgcctgcccg 68700
atcctccgct tccagggttc gattcggcca aggtgacgag ctccgatatc 68750

<210> 2
<211> 1421

<212> PRT
<213> Sorangium cellulosum

<400> 2

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Val Ala Asp Arg Pro Ile Glu Arg Ala Ala Glu Asp Pro Ile Ala Ile
  1               5                  10                  15

Val Gly Ala Ser Cys Arg Leu Pro Gly Gly Val Ile Asp Leu Ser Gly
            20                  25                  30

Phe Trp Thr Leu Leu Glu Gly Ser Arg Asp Thr Val Gly Arg Val Pro
        35                  40                  45

Ala Glu Arg Trp Asp Ala Ala Ala Trp Phe Asp Pro Asp Pro Asp Ala
    50                  55                  60

Pro Gly Lys Thr Pro Val Thr Arg Ala Ser Phe Leu Ser Asp Val Ala
65                  70                  75                  80

Cys Phe Asp Ala Ser Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Arg
                85                  90                  95

Met Asp Pro Ala His Arg Leu Leu Leu Glu Val Cys Trp Glu Ala Leu
            100                 105                 110

Glu Asn Ala Ala Ile Ala Pro Ser Ala Leu Val Gly Thr Glu Thr Gly
        115                 120                 125

Val Phe Ile Gly Ile Gly Pro Ser Glu Tyr Glu Ala Ala Leu Pro Gln
    130                 135                 140

Ala Thr Ala Ser Ala Glu Ile Asp Ala His Gly Gly Leu Gly Thr Met
145                 150                 155                 160

Pro Ser Val Gly Ala Gly Arg Ile Ser Tyr Ala Leu Gly Leu Arg Gly
                165                 170                 175

Pro Cys Val Ala Val Asp Thr Ala Tyr Ser Ser Ser Leu Val Ala Val
            180                 185                 190

His Leu Ala Cys Gln Ser Leu Arg Ser Gly Glu Cys Ser Thr Ala Leu
        195                 200                 205

Ala Gly Gly Val Ser Leu Met Leu Ser Pro Ser Thr Leu Val Trp Leu
    210                 215                 220

Ser Lys Thr Arg Ala Leu Ala Arg Asp Gly Arg Cys Lys Ala Phe Ser
225                 230                 235                 240

Ala Glu Ala Asp Gly Phe Gly Arg Gly Glu Gly Cys Ala Val Val Val
                245                 250                 255

Leu Lys Arg Leu Ser Gly Ala Arg Ala Asp Gly Asp Arg Ile Leu Ala
            260                 265                 270

Val Ile Arg Gly Ser Ala Ile Asn His Asp Gly Ala Ser Ser Gly Leu
        275                 280                 285

Thr Val Pro Asn Gly Ser Ser Gln Glu Ile Val Leu Lys Arg Ala Leu
    290                 295                 300

Ala Asp Ala Gly Cys Ala Ala Ser Ser Val Gly Tyr Val Glu Ala His
305                 310                 315                 320

Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile Glu Ile Gln Ala Leu Asn
```

325 330 335

Ala Val Tyr Gly Leu Gly Arg Asp Val Ala Thr Pro Leu Leu Ile Gly
340 345 350

Ser Val Lys Thr Asn Leu Gly His Pro Glu Tyr Ala Ser Gly Ile Thr
355 360 365

Gly Leu Leu Lys Val Val Leu Ser Leu Gln His Gly Gln Ile Pro Ala
370 375 380

His Leu His Ala Gln Ala Leu Asn Pro Arg Ile Ser Trp Gly Asp Leu
385 390 395 400

Arg Leu Thr Val Thr Arg Ala Arg Thr Pro Trp Pro Asp Trp Asn Thr
405 410 415

Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Met Ser Gly Thr Asn Ala
420 425 430

His Val Val Leu Glu Glu Ala Pro Ala Ala Thr Cys Thr Pro Pro Ala
435 440 445

Pro Glu Arg Pro Ala Glu Leu Leu Val Leu Ser Ala Arg Thr Ala Ser
450 455 460

Ala Leu Asp Ala Gln Ala Ala Arg Leu Arg Asp His Leu Glu Thr Tyr
465 470 475 480

Pro Ser Gln Cys Leu Gly Asp Val Ala Phe Ser Leu Ala Thr Thr Arg
485 490 495

Ser Ala Met Glu His Arg Leu Ala Val Ala Ala Thr Ser Arg Glu Gly
500 505 510

Leu Arg Ala Ala Leu Asp Ala Ala Ala Gln Gly Gln Thr Ser Pro Gly
515 520 525

Ala Val Arg Ser Ile Ala Asp Ser Ser Arg Gly Lys Leu Ala Phe Leu
530 535 540

Phe Thr Gly Gln Gly Ala Gln Thr Leu Gly Met Gly Arg Gly Leu Tyr
545 550 555 560

Asp Val Trp Ser Ala Phe Arg Glu Ala Phe Asp Leu Cys Val Arg Leu
565 570 575

Phe Asn Gln Glu Leu Asp Arg Pro Leu Arg Glu Val Met Trp Ala Glu
580 585 590

Pro Ala Ser Val Asp Ala Ala Leu Leu Asp Gln Thr Ala Phe Thr Gln
595 600 605

Pro Ala Leu Phe Thr Phe Glu Tyr Ala Leu Ala Ala Leu Trp Arg Ser
610 615 620

Trp Gly Val Glu Pro Glu Leu Val Ala Gly His Ser Ile Gly Glu Leu
625 630 635 640

Val Ala Ala Cys Val Ala Gly Val Phe Ser Leu Glu Asp Ala Val Phe
645 650 655

Leu Val Ala Ala Arg Gly Arg Leu Met Gln Ala Leu Pro Ala Gly Gly
660 665 670

Ala Met Val Ser Ile Glu Ala Pro Glu Ala Asp Val Ala Ala Ala Val
675 680 685

Ala Pro His Ala Ala Ser Val Ser Ile Ala Ala Val Asn Ala Pro Asp
690 695 700

Gln Val Val Ile Ala Gly Ala Gly Gln Pro Val His Ala Ile Ala Ala
705 710 715 720

Ala Met Ala Ala Arg Gly Ala Arg Thr Lys Ala Leu His Val Ser His
725 730 735

Ala Phe His Ser Pro Leu Met Ala Pro Met Leu Glu Ala Phe Gly Arg
740 745 750

Val Ala Glu Ser Val Ser Tyr Arg Arg Pro Ser Ile Val Leu Val Ser
755 760 765

Asn Leu Ser Gly Lys Ala Cys Thr Asp Glu Val Ser Ser Pro Gly Tyr
770 775 780

Trp Val Arg His Ala Arg Glu Val Val Arg Phe Ala Asp Gly Val Lys
785 790 795 800

Ala Leu His Ala Ala Gly Ala Gly Thr Phe Val Glu Val Gly Pro Lys
805 810 815

Ser Thr Leu Leu Gly Leu Val Pro Ala Cys Met Pro Asp Ala Arg Pro
820 825 830

Ala Leu Leu Ala Ser Ser Arg Ala Gly Arg Asp Glu Pro Ala Thr Val
835 840 845

Leu Glu Ala Leu Gly Gly Leu Trp Ala Val Gly Gly Leu Val Ser Trp
850 855 860

Ala Gly Leu Phe Pro Ser Gly Gly Arg Arg Val Pro Leu Pro Thr Tyr
865 870 875 880

Pro Trp Gln Arg Glu Arg Tyr Trp Ile Asp Thr Lys Ala Asp Asp Ala
885 890 895

Ala Arg Gly Asp Arg Arg Ala Pro Gly Ala Gly His Asp Glu Val Glu
900 905 910

Glu Gly Gly Ala Val Arg Gly Gly Asp Arg Arg Ser Ala Arg Leu Asp
915 920 925

His Pro Pro Pro Glu Ser Gly Arg Arg Glu Lys Val Glu Ala Ala Gly
930 935 940

Asp Arg Pro Phe Arg Leu Glu Ile Asp Glu Pro Gly Val Leu Asp His
945 950 955 960

Leu Val Leu Arg Val Thr Glu Arg Arg Ala Pro Gly Leu Gly Glu Val
965 970 975

Glu Ile Ala Val Asp Ala Ala Gly Leu Ser Phe Asn Asp Val Gln Leu
980 985 990

Ala Leu Gly Met Val Pro Asp Asp Leu Pro Gly Lys Pro Asn Pro Pro
995 1000 1005

Leu Leu Leu Gly Gly Glu Cys Ala Gly Arg Ile Val Ala Val Gly Glu
1010 1015 1020

```
Gly Val Asn Gly Leu Val Val Gly Gln Pro Val Ile Ala Leu Ser Ala
1025                1030                1035                1040

Gly Ala Phe Ala Thr His Val Thr Thr Ser Ala Ala Leu Val Leu Pro
                1045                1050                1055

Arg Pro Gln Ala Leu Ser Ala Ile Glu Ala Ala Ala Met Pro Val Ala
            1060                1065                1070

Tyr Leu Thr Ala Trp Tyr Ala Leu Asp Arg Ile Ala Arg Leu Gln Pro
        1075                1080                1085

Gly Glu Arg Val Leu Ile His Ala Ala Thr Gly Gly Val Gly Leu Ala
    1090                1095                1100

Ala Val Gln Trp Ala Gln His Val Gly Ala Glu Val His Ala Thr Ala
1105                1110                1115                1120

Gly Thr Pro Glu Lys Arg Ala Tyr Leu Glu Ser Leu Gly Val Arg Tyr
                1125                1130                1135

Val Ser Asp Ser Arg Ser Asp Arg Phe Val Ala Asp Val Arg Ala Trp
            1140                1145                1150

Thr Gly Gly Glu Gly Val Asp Val Val Leu Asn Ser Leu Ser Gly Glu
        1155                1160                1165

Leu Ile Asp Lys Ser Phe Asn Leu Leu Arg Ser His Gly Arg Phe Val
    1170                1175                1180

Glu Leu Gly Lys Arg Asp Cys Tyr Ala Asp Asn Gln Leu Gly Leu Arg
1185                1190                1195                1200

Pro Phe Leu Arg Asn Leu Ser Phe Ser Leu Val Asp Leu Arg Gly Met
                1205                1210                1215

Met Leu Glu Arg Pro Ala Arg Val Arg Ala Leu Leu Glu Glu Leu Leu
            1220                1225                1230

Gly Leu Ile Ala Ala Gly Val Phe Thr Pro Pro Pro Ile Ala Thr Leu
        1235                1240                1245

Pro Ile Ala Arg Val Ala Asp Ala Phe Arg Ser Met Ala Gln Ala Gln
    1250                1255                1260

His Leu Gly Lys Leu Val Leu Thr Leu Gly Asp Pro Glu Val Gln Ile
1265                1270                1275                1280

Arg Ile Pro Thr His Ala Gly Ala Gly Pro Ser Thr Gly Asp Arg Asp
                1285                1290                1295

Leu Leu Asp Arg Leu Ala Ser Ala Ala Pro Ala Ala Arg Ala Ala Ala
            1300                1305                1310

Leu Glu Ala Phe Leu Arg Thr Gln Val Ser Gln Val Leu Arg Thr Pro
        1315                1320                1325

Glu Ile Lys Val Gly Ala Glu Ala Leu Phe Thr Arg Leu Gly Met Asp
    1330                1335                1340

Ser Leu Met Ala Val Glu Leu Arg Asn Arg Ile Glu Ala Ser Leu Lys
1345                1350                1355                1360

Leu Lys Leu Ser Thr Thr Phe Leu Ser Thr Ser Pro Asn Ile Ala Leu
```

1365 1370 1375

Leu Ala Gln Asn Leu Leu Asp Ala Leu Ala Thr Ala Leu Ser Leu Glu
1380 1385 1390

Arg Val Ala Ala Glu Asn Leu Arg Ala Gly Val Gln Asn Asp Phe Val
1395 1400 1405

Ser Ser Gly Ala Asp Gln Asp Trp Glu Ile Ile Ala Leu
1410 1415 1420

<210> 3
<211> 1410
<212> PRT
<213> Sorangium cellulosum

<400> 3
Met Thr Ile Asn Gln Leu Leu Asn Glu Leu Glu His Gln Gly Ile Lys
1 5 10 15

Leu Ala Ala Asp Gly Glu Arg Leu Gln Ile Gln Ala Pro Lys Asn Ala
20 25 30

Leu Asn Pro Asn Leu Leu Ala Arg Ile Ser Glu His Lys Ser Thr Ile
35 40 45

Leu Thr Met Leu Arg Gln Arg Leu Pro Ala Glu Ser Ile Val Pro Ala
50 55 60

Pro Ala Glu Arg His Ala Pro Phe Pro Leu Thr Asp Ile Gln Glu Ser
65 70 75 80

Tyr Trp Leu Gly Arg Thr Gly Ala Phe Thr Val Pro Ser Gly Ile His
85 90 95

Ala Tyr Arg Glu Tyr Asp Cys Thr Asp Leu Asp Val Pro Arg Leu Ser
100 105 110

Arg Ala Phe Arg Lys Val Val Ala Arg His Asp Met Leu Arg Ala His
115 120 125

Thr Leu Pro Asp Met Met Gln Val Ile Glu Pro Lys Val Asp Ala Asp
130 135 140

Ile Glu Ile Ile Asp Leu Arg Gly Leu Asp Arg Ser Thr Arg Glu Ala
145 150 155 160

Arg Leu Val Ser Leu Arg Asp Ala Met Ser His Arg Ile Tyr Asp Thr
165 170 175

Glu Arg Pro Pro Leu Tyr His Val Val Ala Val Arg Leu Asp Glu Arg
180 185 190

Gln Thr Arg Leu Val Leu Ser Ile Asp Leu Ile Asn Val Asp Leu Gly
195 200 205

Ser Leu Ser Ile Ile Phe Lys Asp Trp Leu Ser Phe Tyr Glu Asp Pro
210 215 220

Glu Thr Ser Leu Pro Val Leu Glu Leu Ser Tyr Arg Asp Tyr Val Leu
225 230 235 240

Ala Leu Glu Ser Arg Lys Lys Ser Glu Ala His Gln Arg Ser Met Asp
245 250 255

Tyr Trp Lys Arg Arg Ile Ala Glu Leu Pro Pro Pro Pro Thr Leu Pro
260 265 270

Met Lys Ala Asp Pro Ser Thr Leu Lys Glu Ile Arg Phe Arg His Thr
275 280 285

Glu Gln Trp Leu Pro Ser Asp Ser Trp Gly Arg Leu Lys Arg Arg Val
290 295 300

Gly Glu Arg Gly Leu Thr Pro Thr Gly Val Ile Leu Ala Ala Phe Ser
305 310 315 320

Glu Val Ile Gly Arg Trp Ser Ala Ser Pro Arg Phe Thr Leu Asn Ile
325 330 335

Thr Leu Phe Asn Arg Leu Pro Val His Pro Arg Val Asn Asp Ile Thr
340 345 350

Gly Asp Phe Thr Ser Met Val Leu Leu Asp Ile Asp Thr Thr Arg Asp
355 360 365

Lys Ser Phe Glu Gln Arg Ala Lys Arg Ile Gln Glu Gln Leu Trp Glu
370 375 380

Ala Met Asp His Cys Asp Val Ser Gly Ile Glu Val Gln Arg Glu Ala
385 390 395 400

Ala Arg Val Leu Gly Ile Gln Arg Gly Ala Leu Phe Pro Val Val Leu
405 410 415

Thr Ser Ala Leu Asn Gln Gln Val Val Gly Val Thr Ser Leu Gln Arg
420 425 430

Leu Gly Thr Pro Val Tyr Thr Ser Thr Gln Thr Pro Gln Leu Leu Leu
435 440 445

Asp His Gln Leu Tyr Glu His Asp Gly Asp Leu Val Leu Ala Trp Asp
450 455 460

Ile Val Asp Gly Val Phe Pro Pro Asp Leu Leu Asp Asp Met Leu Glu
465 470 475 480

Ala Tyr Val Val Phe Leu Arg Arg Leu Thr Glu Glu Pro Trp Gly Glu
485 490 495

Gln Val Arg Cys Ser Leu Pro Pro Ala Gln Leu Glu Ala Arg Ala Ser
500 505 510

Ala Asn Ala Thr Asn Ala Leu Leu Ser Glu His Thr Leu His Gly Leu
515 520 525

Phe Ala Ala Arg Val Glu Gln Leu Pro Met Gln Leu Ala Val Val Ser
530 535 540

Ala Arg Lys Thr Leu Thr Tyr Glu Glu Leu Ser Arg Arg Ser Arg Arg
545 550 555 560

Leu Gly Ala Arg Leu Arg Glu Gln Gly Ala Arg Pro Asn Thr Leu Val
565 570 575

Ala Val Val Met Glu Lys Gly Trp Glu Gln Val Val Ala Val Leu Ala
580 585 590

Val Leu Glu Ser Gly Ala Ala Tyr Val Pro Ile Asp Ala Asp Leu Pro

595 600 605

Ala Glu Arg Ile His Tyr Leu Leu Asp His Gly Glu Val Lys Leu Val
610 615 620

Leu Thr Gln Pro Trp Leu Asp Gly Lys Leu Ser Trp Pro Pro Gly Ile
625 630 635 640

Gln Arg Leu Leu Val Ser Glu Ala Gly Val Glu Gly Asp Gly Asp Gln
645 650 655

Pro Pro Met Met Pro Ile Gln Thr Pro Ser Asp Leu Ala Tyr Val Ile
660 665 670

Tyr Thr Ser Gly Ser Thr Gly Leu Pro Lys Gly Val Met Ile Asp His
675 680 685

Arg Gly Ala Val Asn Thr Ile Leu Asp Ile Asn Glu Arg Phe Glu Ile
690 695 700

Gly Pro Gly Asp Arg Val Leu Ala Leu Ser Ser Leu Ser Phe Asp Leu
705 710 715 720

Ser Val Tyr Asp Val Phe Gly Ile Leu Ala Ala Gly Gly Thr Ile Val
725 730 735

Val Pro Asp Ala Ser Lys Leu Arg Asp Pro Ala His Trp Ala Glu Leu
740 745 750

Ile Glu Arg Glu Lys Val Thr Val Trp Asn Ser Val Pro Ala Leu Met
755 760 765

Arg Met Leu Val Glu His Phe Glu Gly Arg Pro Asp Ser Leu Ala Arg
770 775 780

Ser Leu Arg Leu Ser Leu Leu Ser Gly Asp Trp Ile Pro Val Gly Leu
785 790 795 800

Pro Gly Glu Leu Gln Ala Ile Arg Pro Gly Val Ser Val Ile Ser Leu
805 810 815

Gly Gly Ala Thr Glu Ala Ser Ile Trp Ser Ile Gly Tyr Pro Val Arg
820 825 830

Asn Val Asp Leu Ser Trp Ala Ser Ile Pro Tyr Gly Arg Pro Leu Arg
835 840 845

Asn Gln Thr Phe His Val Leu Asp Glu Ala Leu Glu Pro Arg Pro Val
850 855 860

Trp Val Pro Gly Gln Leu Tyr Ile Gly Gly Val Gly Leu Ala Leu Gly
865 870 875 880

Tyr Trp Arg Asp Glu Glu Lys Thr Arg Lys Ser Phe Leu Val His Pro
885 890 895

Glu Thr Gly Glu Arg Leu Tyr Lys Thr Gly Asp Leu Gly Arg Tyr Leu
900 905 910

Pro Asp Gly Asn Ile Glu Phe Met Gly Arg Glu Asp Asn Gln Ile Lys
915 920 925

Leu Arg Gly Tyr Arg Val Glu Leu Gly Glu Ile Glu Glu Thr Leu Lys
930 935 940

Ser His Pro Asn Val Arg Asp Ala Val Ile Val Pro Val Gly Asn Asp
945 950 955 960

Ala Ala Asn Lys Leu Leu Leu Ala Tyr Val Val Pro Glu Gly Thr Arg
965 970 975

Arg Arg Ala Ala Glu Gln Asp Ala Ser Leu Lys Thr Glu Arg Ile Asp
980 985 990

Ala Arg Ala His Ala Ala Glu Ala Asp Gly Leu Ser Asp Gly Glu Arg
995 1000 1005

Val Gln Phe Lys Leu Ala Arg His Gly Leu Arg Arg Asp Leu Asp Gly
1010 1015 1020

Lys Pro Val Val Asp Leu Thr Gly Gln Asp Pro Arg Glu Ala Gly Leu
1025 1030 1035 1040

Asp Val Tyr Ala Arg Arg Arg Ser Val Arg Thr Phe Leu Glu Ala Pro
1045 1050 1055

Ile Pro Phe Val Glu Phe Gly Arg Phe Leu Ser Cys Leu Ser Ser Val
1060 1065 1070

Glu Pro Asp Gly Ala Thr Leu Pro Lys Phe Arg Tyr Pro Ser Ala Gly
1075 1080 1085

Ser Thr Tyr Pro Val Gln Thr Tyr Ala Tyr Val Lys Ser Gly Arg Ile
1090 1095 1100

Glu Gly Val Asp Glu Gly Phe Tyr Tyr Tyr His Pro Phe Glu His Arg
1105 1110 1115 1120

Leu Leu Lys Leu Ser Asp His Gly Ile Glu Arg Gly Ala His Val Arg
1125 1130 1135

Gln Asn Phe Asp Val Phe Asp Glu Ala Ala Phe Asn Leu Leu Phe Val
1140 1145 1150

Gly Arg Ile Asp Ala Ile Glu Ser Leu Tyr Gly Ser Ser Ser Arg Glu
1155 1160 1165

Phe Cys Leu Leu Glu Ala Gly Tyr Met Ala Gln Leu Leu Met Glu Gln
1170 1175 1180

Ala Pro Ser Cys Asn Ile Gly Val Cys Pro Val Gly Gln Phe Asn Phe
1185 1190 1195 1200

Glu Gln Val Arg Pro Val Leu Asp Leu Arg His Ser Asp Val Tyr Val
1205 1210 1215

His Gly Met Leu Gly Gly Arg Val Asp Pro Arg Gln Phe Gln Val Cys
1220 1225 1230

Thr Leu Gly Gln Asp Ser Ser Pro Arg Arg Ala Thr Thr Arg Gly Ala
1235 1240 1245

Pro Pro Gly Arg Glu Gln His Phe Ala Asp Met Leu Arg Asp Phe Leu
1250 1255 1260

Arg Thr Lys Leu Pro Glu Tyr Met Val Pro Thr Val Phe Val Glu Leu
1265 1270 1275 1280

Asp Ala Leu Pro Leu Thr Ser Asn Gly Lys Val Asp Arg Lys Ala Leu
1285 1290 1295

```
Arg Glu Arg Lys Asp Thr Ser Ser Pro Arg His Ser Gly His Thr Ala
          1300                1305                1310

Pro Arg Asp Ala Leu Glu Glu Ile Leu Val Ala Val Val Arg Glu Val
      1315                1320                1325

Leu Gly Leu Glu Val Val Gly Leu Gln Gln Ser Phe Val Asp Leu Gly
   1330                1335                1340

Ala Thr Ser Ile His Ile Val Arg Met Arg Ser Leu Leu Gln Lys Arg
1345                1350                1355                1360

Leu Asp Arg Glu Ile Ala Ile Thr Glu Leu Phe Gln Tyr Pro Asn Leu
               1365                1370                1375

Gly Ser Leu Ala Ser Gly Leu Arg Arg Asp Ser Arg Asp Leu Asp Gln
          1380                1385                1390

Arg Pro Asn Met Gln Asp Arg Val Glu Val Arg Arg Lys Gly Arg Arg
      1395                1400                1405

Arg Ser
   1410
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<210> 4
<211> 1832
<212> PRT
<213> Sorangium cellulosum

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<400> 4
Met Glu Glu Gln Glu Ser Ser Ala Ile Ala Val Ile Gly Met Ser Gly
  1               5                  10                  15

Arg Phe Pro Gly Ala Arg Asp Leu Asp Glu Phe Trp Arg Asn Leu Arg
             20                  25                  30

Asp Gly Thr Glu Ala Val Gln Arg Phe Ser Glu Gln Glu Leu Ala Ala
         35                  40                  45

Ser Gly Val Asp Pro Ala Leu Val Leu Asp Pro Ser Tyr Val Arg Ala
     50                  55                  60

Gly Ser Val Leu Glu Asp Val Asp Arg Phe Asp Ala Ala Phe Phe Gly
 65                  70                  75                  80

Ile Ser Pro Arg Glu Ala Glu Leu Met Asp Pro Gln His Arg Ile Phe
                 85                  90                  95

Met Glu Cys Ala Trp Glu Ala Leu Glu Asn Ala Gly Tyr Asp Pro Thr
            100                 105                 110

Ala Tyr Glu Gly Ser Ile Gly Val Tyr Ala Gly Ala Asn Met Ser Ser
        115                 120                 125

Tyr Leu Thr Ser Asn Leu His Glu His Pro Ala Met Met Arg Trp Pro
    130                 135                 140

Gly Trp Phe Gln Thr Leu Ile Gly Asn Asp Lys Asp Tyr Leu Ala Thr
145                 150                 155                 160

His Val Ser Tyr Arg Leu Asn Leu Arg Gly Pro Ser Ile Ser Val Gln
                165                 170                 175
```

Thr Ala Cys Ser Thr Ser Leu Val Ala Val His Leu Ala Cys Met Ser
180 185 190

Leu Leu Asp Arg Glu Cys Asp Met Ala Leu Ala Gly Gly Ile Thr Val
195 200 205

Arg Ile Pro His Arg Ala Gly Tyr Val Tyr Ala Glu Gly Gly Ile Phe
210 215 220

Ser Pro Asp Gly His Cys Arg Ala Phe Asp Ala Lys Ala Asn Gly Thr
225 230 235 240

Ile Met Gly Asn Gly Cys Gly Val Val Leu Leu Lys Pro Leu Asp Arg
245 250 255

Ala Leu Ser Asp Gly Asp Pro Val Arg Ala Val Ile Leu Gly Ser Ala
260 265 270

Thr Asn Asn Asp Gly Ala Arg Lys Ile Gly Phe Thr Ala Pro Ser Glu
275 280 285

Val Gly Gln Ala Gln Ala Ile Met Glu Ala Leu Ala Leu Ala Gly Val
290 295 300

Glu Ala Arg Ser Ile Gln Tyr Ile Glu Thr His Gly Thr Gly Thr Leu
305 310 315 320

Leu Gly Asp Ala Ile Glu Thr Ala Ala Leu Arg Arg Val Phe Gly Arg
325 330 335

Asp Ala Ser Ala Arg Arg Ser Cys Ala Ile Gly Ser Val Lys Thr Gly
340 345 350

Ile Gly His Leu Glu Ser Ala Ala Gly Ile Ala Gly Leu Ile Lys Thr
355 360 365

Val Leu Ala Leu Glu His Arg Gln Leu Pro Pro Ser Leu Asn Phe Glu
370 375 380

Ser Pro Asn Pro Ser Ile Asp Phe Ala Ser Ser Pro Phe Tyr Val Asn
385 390 395 400

Thr Ser Leu Lys Asp Trp Asn Thr Gly Ser Thr Pro Arg Arg Ala Gly
405 410 415

Val Ser Ser Phe Gly Ile Gly Gly Thr Asn Ala His Val Val Leu Glu
420 425 430

Glu Ala Pro Ala Ala Lys Leu Pro Ala Ala Ala Pro Ala Arg Ser Ala
435 440 445

Glu Leu Phe Val Val Ser Ala Lys Ser Ala Ala Ala Leu Asp Ala Ala
450 455 460

Ala Ala Arg Leu Arg Asp His Leu Gln Ala His Gln Gly Ile Ser Leu
465 470 475 480

Gly Asp Val Ala Phe Ser Leu Ala Thr Thr Arg Ser Pro Met Glu His
485 490 495

Arg Leu Ala Met Ala Ala Pro Ser Arg Glu Ala Leu Arg Glu Gly Leu
500 505 510

Asp Ala Ala Ala Arg Gly Gln Thr Pro Pro Gly Ala Val Arg Gly Arg
515 520 525

```
Cys Ser Pro Gly Asn Val Pro Lys Val Val Phe Val Phe Pro Gly Gln
    530                 535                 540

Gly Ser Gln Trp Val Gly Met Gly Arg Gln Leu Leu Ala Glu Glu Pro
545                 550                 555                 560

Val Phe His Ala Ala Leu Ser Ala Cys Asp Arg Ala Ile Gln Ala Glu
                565                 570                 575

Ala Gly Trp Ser Leu Leu Ala Glu Leu Ala Ala Asp Glu Gly Ser Ser
            580                 585                 590

Gln Leu Glu Arg Ile Asp Val Val Gln Pro Val Leu Phe Ala Leu Ala
        595                 600                 605

Val Ala Phe Ala Ala Leu Trp Arg Ser Trp Gly Val Ala Pro Asp Val
    610                 615                 620

Val Ile Gly His Ser Met Gly Glu Val Ala Ala Ala His Val Ala Gly
625                 630                 635                 640

Ala Leu Ser Leu Glu Asp Ala Val Ala Ile Ile Cys Arg Arg Ser Arg
                645                 650                 655

Leu Leu Arg Arg Ile Ser Gly Gln Gly Glu Met Ala Val Thr Glu Leu
            660                 665                 670

Ser Leu Ala Glu Ala Glu Ala Ala Leu Arg Gly Tyr Glu Asp Arg Val
        675                 680                 685

Ser Val Ala Val Ser Asn Ser Pro Arg Ser Thr Val Leu Ser Gly Glu
    690                 695                 700

Pro Ala Ala Ile Gly Glu Val Leu Ser Ser Leu Asn Ala Lys Gly Val
705                 710                 715                 720

Phe Cys Arg Arg Val Lys Val Asp Val Ala Ser His Ser Pro Gln Val
                725                 730                 735

Asp Pro Leu Arg Glu Asp Leu Leu Ala Ala Leu Gly Gly Leu Arg Pro
            740                 745                 750

Gly Ala Ala Ala Val Pro Met Arg Ser Thr Val Thr Gly Ala Met Val
        755                 760                 765

Ala Gly Pro Glu Leu Gly Ala Asn Tyr Trp Met Asn Asn Leu Arg Gln
    770                 775                 780

Pro Val Arg Phe Ala Glu Val Val Gln Ala Gln Leu Gln Gly Gly His
785                 790                 795                 800

Gly Leu Phe Val Glu Met Ser Pro His Pro Ile Leu Thr Thr Ser Val
                805                 810                 815

Glu Glu Met Arg Arg Ala Ala Gln Arg Ala Gly Ala Ala Val Gly Ser
            820                 825                 830

Leu Arg Arg Gly Gln Asp Glu Arg Pro Ala Met Leu Glu Ala Leu Gly
        835                 840                 845

Thr Leu Trp Ala Gln Gly Tyr Pro Val Pro Trp Gly Arg Leu Phe Pro
    850                 855                 860

Ala Gly Gly Arg Arg Val Pro Leu Pro Thr Tyr Pro Trp Gln Arg Glu
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865 870 875 880

Arg Tyr Trp Ile Glu Ala Pro Ala Lys Ser Ala Ala Gly Asp Arg Arg
885 890 895

Gly Val Arg Ala Gly Gly His Pro Leu Leu Gly Glu Met Gln Thr Leu
900 905 910

Ser Thr Gln Thr Ser Thr Arg Leu Trp Glu Thr Thr Leu Asp Leu Lys
915 920 925

Arg Leu Pro Trp Leu Gly Asp His Arg Val Gln Gly Ala Val Val Phe
930 935 940

Pro Gly Ala Ala Tyr Leu Glu Met Ala Ile Ser Ser Gly Ala Glu Ala
945 950 955 960

Leu Gly Asp Gly Pro Leu Gln Ile Thr Asp Val Val Leu Ala Glu Ala
965 970 975

Leu Ala Phe Ala Gly Asp Ala Ala Val Leu Val Gln Val Val Thr Thr
980 985 990

Glu Gln Pro Ser Gly Arg Leu Gln Phe Gln Ile Ala Ser Arg Ala Pro
995 1000 1005

Gly Ala Gly His Ala Ser Phe Arg Val His Ala Arg Gly Ala Leu Leu
1010 1015 1020

Arg Val Glu Arg Thr Glu Val Pro Ala Gly Leu Thr Leu Ser Ala Val
1025 1030 1035 1040

Arg Ala Arg Leu Gln Ala Ser Ile Pro Ala Ala Ala Thr Tyr Ala Glu
1045 1050 1055

Leu Thr Glu Met Gly Leu Gln Tyr Gly Pro Ala Phe Gln Gly Ile Ala
1060 1065 1070

Glu Leu Trp Arg Gly Glu Gly Glu Ala Leu Gly Arg Val Arg Leu Pro
1075 1080 1085

Asp Ala Ala Gly Ser Ala Ala Glu Tyr Arg Leu His Pro Ala Leu Leu
1090 1095 1100

Asp Ala Cys Phe Gln Ile Val Gly Ser Leu Phe Ala Arg Ser Gly Glu
1105 1110 1115 1120

Ala Thr Pro Trp Val Pro Val Glu Leu Gly Ser Leu Arg Leu Leu Gln
1125 1130 1135

Arg Pro Ser Gly Glu Leu Trp Cys His Ala Arg Val Val Asn His Gly
1140 1145 1150

His Gln Thr Pro Asp Arg Gln Gly Ala Asp Phe Trp Val Val Asp Ser
1155 1160 1165

Ser Gly Ala Val Val Ala Glu Val Cys Gly Leu Val Ala Gln Arg Leu
1170 1175 1180

Pro Gly Gly Val Arg Arg Arg Glu Glu Asp Asp Trp Phe Leu Glu Leu
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Glu Trp Glu Pro Ala Ala Val Gly Thr Ala Lys Val Asn Ala Gly Arg
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Trp Leu Leu Leu Gly Gly Gly Gly Gly Leu Gly Ala Ala Leu Arg Ala
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Met Leu Glu Ala Gly Gly His Ala Val Val His Ala Ala Glu Asn Asn
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Thr Ser Ala Ala Gly Val Arg Ala Leu Leu Ala Lys Ala Phe Asp Gly
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Gln Ala Pro Thr Ala Val Val His Leu Gly Ser Leu Asp Gly Gly Gly
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Glu Leu Asp Pro Gly Leu Gly Ala Gln Gly Ala Leu Asp Ala Pro Arg
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Ser Ala Asp Val Ser Pro Asp Ala Leu Asp Pro Ala Leu Val Arg Gly
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Cys Asp Ser Val Leu Trp Thr Val Gln Ala Leu Ala Gly Met Gly Phe
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Arg Asp Ala Pro Arg Leu Trp Leu Leu Thr Arg Gly Ala Gln Ala Val
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Gly Ala Gly Asp Val Ser Val Thr Gln Ala Pro Leu Leu Gly Leu Gly
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Arg Val Ile Ala Met Glu His Ala Asp Leu Arg Cys Ala Arg Val Asp
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Leu Asp Pro Ala Arg Pro Glu Gly Glu Leu Ala Ala Leu Leu Ala Glu
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Leu Leu Ala Asp Asp Ala Glu Ala Glu Val Ala Leu Arg Gly Gly Glu
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Arg Cys Val Ala Arg Ile Val Arg Arg Gln Pro Glu Thr Arg Pro Arg
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Gly Arg Ile Glu Ser Cys Val Pro Thr Asp Val Thr Ile Arg Ala Asp
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Ser Thr Tyr Leu Val Thr Gly Gly Leu Gly Gly Leu Gly Leu Ser Val
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Ala Gly Trp Leu Ala Glu Arg Gly Ala Gly His Leu Val Leu Val Gly
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Arg Ser Gly Ala Ala Ser Val Glu Gln Arg Ala Ala Val Ala Ala Leu
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Glu Ala Arg Gly Ala Arg Val Thr Val Ala Lys Ala Asp Val Ala Asp
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Arg Ala Gln Leu Glu Arg Ile Leu Arg Glu Val Thr Thr Ser Gly Met
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Pro Leu Arg Gly Val Val His Ala Ala Gly Ile Leu Asp Asp Gly Leu
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Leu Met Gln Gln Thr Pro Ala Arg Phe Arg Lys Val Met Ala Pro Lys
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Val Gln Gly Ala Leu His Leu His Ala Leu Thr Arg Glu Ala Pro Leu
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Ser Phe Phe Val Leu Tyr Ala Ser Gly Val Gly Leu Leu Gly Ser Pro
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Gly Gln Gly Asn Tyr Ala Ala Ala Asn Thr Phe Leu Asp Ala Leu Ala
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His His Arg Arg Ala Gln Gly Leu Pro Ala Leu Ser Val Asp Trp Gly
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Leu Phe Ala Glu Val Gly Met Ala Ala Ala Gln Glu Asp Arg Gly Ala
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Arg Leu Val Ser Arg Gly Met Arg Ser Leu Thr Pro Asp Glu Gly Leu
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Ser Ala Leu Ala Arg Leu Leu Glu Ser Gly Arg Ala Gln Val Gly Val
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Met Pro Val Asn Pro Arg Leu Trp Val Glu Leu Tyr Pro Ala Ala Ala
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Ser Ser Arg Met Leu Ser Arg Leu Val Thr Ala His Arg Ala Ser Ala
1685 1690 1695

Gly Gly Pro Ala Gly Asp Gly Asp Leu Leu Arg Arg Leu Ala Ala Ala
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Glu Pro Ser Ala Arg Ser Ala Leu Leu Glu Pro Leu Leu Arg Ala Gln
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Ile Ser Gln Val Leu Arg Leu Pro Glu Gly Lys Ile Glu Val Asp Ala
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Pro Leu Thr Ser Leu Gly Met Asn Ser Leu Met Gly Leu Glu Leu Arg
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Asn Arg Ile Glu Ala Met Leu Gly Ile Thr Val Pro Ala Thr Leu Leu
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Trp Thr Tyr Pro Thr Val Ala Ala Leu Ser Gly His Leu Ala Arg Glu
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Ala Cys Glu Ala Ala Pro Val Glu Ser Pro His Thr Thr Ala Asp Ser
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Ala Ala Lys Phe Lys Ala Leu Thr
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<212> PRT
<213> Sorangium cellulosum

<400> 5
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Ala Ile Ile Ile Gln Arg Leu Glu Glu Arg Leu Ala Gly Leu Ala Gln
20 25 30

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Ala Glu Leu Glu Arg Thr Glu Pro Ile Ala Ile Val Gly Ile Gly Cys
        35                  40                  45

Arg Phe Pro Gly Gly Ala Asp Ala Pro Glu Ala Phe Trp Glu Leu Leu
    50                  55                  60

Asp Ala Glu Arg Asp Ala Val Gln Pro Leu Asp Met Arg Trp Ala Leu
65                  70                  75                  80

Val Gly Val Ala Pro Val Glu Ala Val Pro His Trp Ala Gly Leu Leu
                85                  90                  95

Thr Glu Pro Ile Asp Cys Phe Asp Ala Ala Phe Phe Gly Ile Ser Pro
            100                 105                 110

Arg Glu Ala Arg Ser Leu Asp Pro Gln His Arg Leu Leu Leu Glu Val
        115                 120                 125

Ala Trp Glu Gly Leu Glu Asp Ala Gly Ile Pro Pro Arg Ser Ile Asp
    130                 135                 140

Gly Ser Arg Thr Gly Val Phe Val Gly Ala Phe Thr Ala Asp Tyr Ala
145                 150                 155                 160

Arg Thr Val Ala Arg Leu Pro Arg Glu Glu Arg Asp Ala Tyr Ser Ala
                165                 170                 175

Thr Gly Asn Met Leu Ser Ile Ala Ala Gly Arg Leu Ser Tyr Thr Leu
            180                 185                 190

Gly Leu Gln Gly Pro Cys Leu Thr Val Asp Thr Ala Cys Ser Ser Ser
        195                 200                 205

Leu Val Ala Ile His Leu Ala Cys Arg Ser Leu Arg Ala Gly Glu Ser
    210                 215                 220

Asp Leu Ala Leu Ala Gly Gly Val Ser Ala Leu Leu Ser Pro Asp Met
225                 230                 235                 240

Met Glu Ala Ala Ala Arg Thr Gln Ala Leu Ser Pro Asp Gly Arg Cys
                245                 250                 255

Arg Thr Phe Asp Ala Ser Ala Asn Gly Phe Val Arg Gly Glu Gly Cys
            260                 265                 270

Gly Leu Val Val Leu Lys Arg Leu Ser Asp Ala Gln Arg Asp Gly Asp
        275                 280                 285

Arg Ile Trp Ala Leu Ile Arg Gly Ser Ala Ile Asn His Asp Gly Arg
    290                 295                 300

Ser Thr Gly Leu Thr Ala Pro Asn Val Leu Ala Gln Glu Thr Val Leu
305                 310                 315                 320

Arg Glu Ala Leu Arg Ser Ala His Val Glu Ala Gly Ala Val Asp Tyr
                325                 330                 335

Val Glu Thr His Gly Thr Gly Thr Ser Leu Gly Asp Pro Ile Glu Val
            340                 345                 350

Glu Ala Leu Arg Ala Thr Val Gly Pro Ala Arg Ser Asp Gly Thr Arg
        355                 360                 365

Cys Val Leu Gly Ala Val Lys Thr Asn Ile Gly His Leu Glu Ala Ala
    370                 375                 380
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Ala Gly Val Ala Gly Leu Ile Lys Ala Ala Leu Ser Leu Thr His Glu
385 390 395 400

Arg Ile Pro Arg Asn Leu Asn Phe Arg Thr Leu Asn Pro Arg Ile Arg
405 410 415

Leu Glu Gly Ser Ala Leu Ala Leu Ala Thr Glu Pro Val Pro Trp Pro
420 425 430

Arg Thr Asp Arg Pro Arg Phe Ala Gly Val Ser Ser Phe Gly Met Ser
435 440 445

Gly Thr Asn Ala His Val Val Leu Glu Glu Ala Pro Ala Val Glu Leu
450 455 460

Trp Pro Ala Ala Pro Glu Arg Ser Ala Glu Leu Leu Val Leu Ser Gly
465 470 475 480

Lys Ser Glu Gly Ala Leu Asp Ala Gln Ala Ala Arg Leu Arg Glu His
485 490 495

Leu Asp Met His Pro Glu Leu Gly Leu Gly Asp Val Ala Phe Ser Leu
500 505 510

Ala Thr Thr Arg Ser Ala Met Ser His Arg Leu Ala Val Ala Val Thr
515 520 525

Ser Arg Glu Gly Leu Leu Ala Ala Leu Ser Ala Val Ala Gln Gly Gln
530 535 540

Thr Pro Ala Gly Ala Ala Arg Cys Ile Ala Ser Ser Ser Arg Gly Lys
545 550 555 560

Leu Ala Phe Leu Phe Thr Gly Gln Gly Ala Gln Thr Pro Gly Met Gly
565 570 575

Arg Gly Leu Cys Ala Ala Trp Pro Ala Phe Arg Glu Ala Phe Asp Arg
580 585 590

Cys Val Ala Leu Phe Asp Arg Glu Leu Asp Arg Pro Leu Arg Glu Val
595 600 605

Met Trp Ala Glu Ala Gly Ser Ala Glu Ser Leu Leu Leu Asp Gln Thr
610 615 620

Ala Phe Thr Gln Pro Ala Leu Phe Ala Val Glu Tyr Ala Leu Thr Ala
625 630 635 640

Leu Trp Arg Ser Trp Gly Val Glu Pro Glu Leu Leu Val Gly His Ser
645 650 655

Ile Gly Glu Leu Val Ala Ala Cys Val Ala Gly Val Phe Ser Leu Glu
660 665 670

Asp Gly Val Arg Leu Val Ala Ala Arg Gly Arg Leu Met Gln Gly Leu
675 680 685

Ser Ala Gly Gly Ala Met Val Ser Leu Gly Ala Pro Glu Ala Glu Val
690 695 700

Ala Ala Ala Val Ala Pro His Ala Ala Ser Val Ser Ile Ala Ala Val
705 710 715 720

Asn Gly Pro Glu Gln Val Val Ile Ala Gly Val Glu Gln Ala Val Gln

725 730 735

Ala Ile Ala Ala Gly Phe Ala Ala Arg Gly Ala Arg Thr Lys Arg Leu
740 745 750

His Val Ser His Ala Phe His Ser Pro Leu Met Glu Pro Met Leu Glu
755 760 765

Glu Phe Gly Arg Val Ala Ala Ser Val Thr Tyr Arg Arg Pro Ser Val
770 775 780

Ser Leu Val Ser Asn Leu Ser Gly Lys Val Val Thr Asp Glu Leu Ser
785 790 795 800

Ala Pro Gly Tyr Trp Val Arg His Val Arg Glu Ala Val Arg Phe Ala
805 810 815

Asp Gly Val Lys Ala Leu His Glu Ala Gly Ala Gly Thr Phe Val Glu
820 825 830

Val Gly Pro Lys Pro Thr Leu Leu Gly Leu Leu Pro Ala Cys Leu Pro
835 840 845

Glu Ala Glu Pro Thr Leu Leu Ala Ser Leu Arg Ala Gly Arg Glu Glu
850 855 860

Ala Ala Gly Val Leu Glu Ala Leu Gly Arg Leu Trp Ala Ala Gly Gly
865 870 875 880

Ser Val Ser Trp Pro Gly Val Phe Pro Thr Ala Gly Arg Arg Val Pro
885 890 895

Leu Pro Thr Tyr Pro Trp Gln Arg Gln Arg Tyr Trp Ile Glu Ala Pro
900 905 910

Ala Glu Gly Leu Gly Ala Thr Ala Ala Asp Ala Leu Ala Gln Trp Phe
915 920 925

Tyr Arg Val Asp Trp Pro Glu Met Pro Arg Ser Ser Val Asp Ser Arg
930 935 940

Arg Ala Arg Ser Gly Gly Trp Leu Val Leu Ala Asp Arg Gly Gly Val
945 950 955 960

Gly Glu Ala Ala Ala Ala Ala Leu Ser Ser Gln Gly Cys Ser Cys Ala
965 970 975

Val Leu His Ala Pro Ala Glu Ala Ser Ala Val Ala Glu Gln Val Thr
980 985 990

Gln Ala Leu Gly Gly Arg Asn Asp Trp Gln Gly Val Leu Tyr Leu Trp
995 1000 1005

Gly Leu Asp Ala Val Val Glu Ala Gly Ala Ser Ala Glu Glu Val Ala
1010 1015 1020

Lys Val Thr His Leu Ala Ala Ala Pro Val Leu Ala Leu Ile Gln Ala
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Leu Gly Thr Gly Pro Arg Ser Pro Arg Leu Trp Ile Val Thr Arg Gly
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Ala Cys Thr Val Gly Gly Glu Pro Asp Ala Ala Pro Cys Gln Ala Ala
1060 1065 1070

Leu Trp Gly Met Gly Arg Val Ala Ala Leu Glu His Pro Gly Ser Trp
1075 1080 1085

Gly Gly Leu Val Asp Leu Asp Pro Glu Glu Ser Pro Thr Glu Val Glu
1090 1095 1100

Ala Leu Val Ala Glu Leu Leu Ser Pro Asp Ala Glu Asp Gln Leu Ala
1105 1110 1115 1120

Phe Arg Gln Gly Arg Arg Arg Ala Ala Arg Leu Val Ala Ala Pro Pro
1125 1130 1135

Glu Gly Asn Ala Ala Pro Val Ser Leu Ser Ala Glu Gly Ser Tyr Leu
1140 1145 1150

Val Thr Gly Gly Leu Gly Ala Leu Gly Leu Leu Val Ala Arg Trp Leu
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Val Glu Arg Gly Ala Gly His Leu Val Leu Ile Ser Arg His Gly Leu
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Pro Asp Arg Glu Glu Trp Gly Arg Asp Gln Pro Pro Glu Val Arg Ala
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Arg Ile Ala Ala Ile Glu Ala Leu Glu Ala Gln Gly Ala Arg Val Thr
1205 1210 1215

Val Ala Ala Val Asp Val Ala Asp Ala Glu Gly Met Ala Ala Leu Leu
1220 1225 1230

Ala Ala Val Glu Pro Pro Leu Arg Gly Val Val His Ala Ala Gly Leu
1235 1240 1245

Leu Asp Asp Gly Leu Leu Ala His Gln Asp Ala Gly Arg Leu Ala Arg
1250 1255 1260

Val Leu Arg Pro Lys Val Glu Gly Ala Trp Val Leu His Thr Leu Thr
1265 1270 1275 1280

Arg Glu Gln Pro Leu Asp Leu Phe Val Leu Phe Ser Ser Ala Ser Gly
1285 1290 1295

Val Phe Gly Ser Ile Gly Gln Gly Ser Tyr Ala Ala Gly Asn Ala Phe
1300 1305 1310

Leu Asp Ala Leu Ala Asp Leu Arg Arg Thr Gln Gly Leu Ala Ala Leu
1315 1320 1325

Ser Ile Ala Trp Gly Leu Trp Ala Glu Gly Gly Met Gly Ser Gln Ala
1330 1335 1340

Gln Arg Arg Glu His Glu Ala Ser Gly Ile Trp Ala Met Pro Thr Ser
1345 1350 1355 1360

Arg Ala Leu Ala Ala Met Glu Trp Leu Leu Gly Thr Arg Ala Thr Gln
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Arg Val Val Ile Gln Met Asp Trp Ala His Ala Gly Ala Ala Pro Arg
1380 1385 1390

Asp Ala Ser Arg Gly Arg Phe Trp Asp Arg Leu Val Thr Ala Thr Lys
1395 1400 1405

Glu Ala Ser Ser Ser Ala Val Pro Ala Val Glu Arg Trp Arg Asn Ala
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Ser Val Val Glu Thr Arg Ser Ala Leu Tyr Glu Leu Val Arg Gly Val
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Val Ala Gly Val Met Gly Phe Thr Asp Gln Gly Thr Leu Asp Val Arg
1445 1450 1455

Arg Gly Phe Ala Glu Gln Gly Leu Asp Ser Leu Met Ala Val Glu Ile
1460 1465 1470

Arg Lys Arg Leu Gln Gly Glu Leu Gly Met Pro Leu Ser Ala Thr Leu
1475 1480 1485

Ala Phe Asp His Pro Thr Val Glu Arg Leu Val Glu Tyr Leu Leu Ser
1490 1495 1500

Gln Ala Leu Glu Leu Gln Asp Arg Thr Asp Val Arg Ser Val Arg Leu
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Pro Ala Thr Glu Asp Pro Ile Ala Ile Val Gly Ala Ala Cys Arg Phe
1525 1530 1535

Pro Gly Gly Val Glu Asp Leu Glu Ser Tyr Trp Gln Leu Leu Thr Glu
1540 1545 1550

Gly Val Val Val Ser Thr Glu Val Pro Ala Asp Arg Trp Asn Gly Ala
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Asp Gly Arg Val Pro Gly Ser Gly Glu Ala Gln Arg Gln Thr Tyr Val
1570 1575 1580

Pro Arg Gly Gly Phe Leu Arg Glu Val Glu Thr Phe Asp Ala Ala Phe
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Phe His Ile Ser Pro Arg Glu Ala Met Ser Leu Asp Pro Gln Gln Arg
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Leu Leu Leu Glu Val Ser Trp Glu Ala Ile Glu Arg Ala Gly Gln Asp
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Pro Ser Ala Leu Arg Glu Ser Pro Thr Gly Val Phe Val Gly Ala Gly
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Pro Asn Glu Tyr Ala Glu Arg Val Gln Glu Leu Ala Asp Glu Ala Ala
1650 1655 1660

Gly Leu Tyr Ser Gly Thr Gly Asn Met Leu Ser Val Ala Ala Gly Arg
1665 1670 1675 1680

Leu Ser Phe Phe Leu Gly Leu His Gly Pro Thr Leu Ala Val Asp Thr
1685 1690 1695

Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Gly Cys Gln Ser Leu
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Arg Arg Gly Glu Cys Asp Gln Ala Leu Val Gly Gly Val Asn Met Leu
1715 1720 1725

Leu Ser Pro Lys Thr Phe Ala Leu Leu Ser Arg Met His Ala Leu Ser
1730 1735 1740

Pro Gly Gly Arg Cys Lys Thr Phe Ser Ala Asp Ala Asp Gly Tyr Ala
1745 1750 1755 1760

Arg Ala Glu Gly Cys Ala Val Val Val Leu Lys Arg Leu Ser Asp Ala

1765 1770 1775

Gln Arg Asp Arg Asp Pro Ile Leu Ala Val Ile Arg Gly Thr Ala Ile
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Asn His Asp Gly Pro Ser Ser Gly Leu Thr Val Pro Ser Gly Pro Ala
1795 1800 1805

Gln Glu Ala Leu Leu Arg Gln Ala Leu Ala His Ala Gly Val Val Pro
1810 1815 1820

Ala Asp Val Asp Phe Val Glu Cys His Gly Thr Gly Thr Ala Leu Gly
1825 1830 1835 1840

Asp Pro Ile Glu Val Arg Ala Leu Ser Asp Val Tyr Gly Gln Ala Arg
1845 1850 1855

Pro Ala Asp Arg Pro Leu Ile Leu Gly Ala Ala Lys Ala Asn Leu Gly
1860 1865 1870

His Met Glu Pro Ala Ala Gly Leu Ala Gly Leu Leu Lys Ala Val Leu
1875 1880 1885

Ala Leu Gly Gln Glu Gln Ile Pro Ala Gln Pro Glu Leu Gly Glu Leu
1890 1895 1900

Asn Pro Leu Leu Pro Trp Glu Ala Leu Pro Val Ala Val Ala Arg Ala
1905 1910 1915 1920

Ala Val Pro Trp Pro Arg Thr Asp Arg Pro Arg Phe Ala Gly Val Ser
1925 1930 1935

Ser Phe Gly Met Ser Gly Thr Asn Ala His Val Val Leu Glu Glu Ala
1940 1945 1950

Pro Ala Val Glu Leu Trp Pro Ala Ala Pro Glu Arg Ser Ala Glu Leu
1955 1960 1965

Leu Val Leu Ser Gly Lys Ser Glu Gly Ala Leu Asp Ala Gln Ala Ala
1970 1975 1980

Arg Leu Arg Glu His Leu Asp Met His Pro Glu Leu Gly Leu Gly Asp
1985 1990 1995 2000

Val Ala Phe Ser Leu Ala Thr Thr Arg Ser Ala Met Asn His Arg Leu
2005 2010 2015

Ala Val Ala Val Thr Ser Arg Glu Gly Leu Leu Ala Ala Leu Ser Ala
2020 2025 2030

Val Ala Gln Gly Gln Thr Pro Pro Gly Ala Ala Arg Cys Ile Ala Ser
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Ser Ser Arg Gly Lys Leu Ala Phe Leu Phe Thr Gly Gln Gly Ala Gln
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Thr Pro Gly Met Gly Arg Gly Leu Cys Ala Ala Trp Pro Ala Phe Arg
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Glu Ala Phe Asp Arg Cys Val Ala Leu Phe Asp Arg Glu Leu Asp Arg
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Pro Leu Arg Glu Val Met Trp Ala Glu Pro Gly Ser Ala Glu Ser Leu
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Leu Leu Asp Gln Thr Ala Phe Thr Gln Pro Ala Leu Phe Thr Val Glu
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Tyr Ala Leu Thr Ala Leu Trp Arg Ser Trp Gly Val Glu Pro Glu Leu
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Val Ala Gly His Ser Ala Gly Glu Leu Val Ala Ala Cys Val Ala Gly
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Val Phe Ser Leu Glu Asp Gly Val Arg Leu Val Ala Ala Arg Gly Arg
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Leu Met Gln Gly Leu Ser Ala Gly Gly Ala Met Val Ser Leu Gly Ala
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Pro Glu Ala Glu Val Ala Ala Ala Val Ala Pro His Ala Ala Ser Val
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Ser Ile Ala Ala Val Asn Gly Pro Glu Gln Val Val Ile Ala Gly Val
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Glu Gln Ala Val Gln Ala Ile Ala Ala Gly Phe Ala Ala Arg Gly Ala
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Arg Thr Lys Arg Leu His Val Ser His Ala Ser His Ser Pro Leu Met
2245 2250 2255

Glu Pro Met Leu Glu Glu Phe Gly Arg Val Ala Ala Ser Val Thr Tyr
2260 2265 2270

Arg Arg Pro Ser Val Ser Leu Val Ser Asn Leu Ser Gly Lys Val Val
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Ala Asp Glu Leu Ser Ala Pro Gly Tyr Trp Val Arg His Val Arg Glu
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2305 2310 2315 2320

Gly Thr Phe Val Glu Val Gly Pro Lys Pro Thr Leu Leu Gly Leu Leu
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Pro Ala Cys Leu Pro Glu Ala Glu Pro Thr Leu Leu Ala Ser Leu Arg
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Ala Gly Arg Glu Glu Ala Ala Gly Val Leu Glu Ala Leu Gly Arg Leu
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Leu Gln Lys Ser Glu Glu Ala Ser Arg Gly Ser Trp Leu Val Leu Ala
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Asp Lys Gly Gly Val Gly Glu Ala Val Ala Ala Ala Leu Ser Thr Arg
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Val Leu Tyr Leu Trp Gly Leu Asp Ala Val Val Gly Ala Glu Ala Ser
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Ile Asp Glu Ile Gly Asp Ala Thr Arg Arg Ala Thr Ala Pro Val Leu
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Gly Leu Ala Arg Phe Leu Ser Thr Val Ser Cys Ser Pro Arg Leu Trp
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Val Val Thr Arg Gly Ala Cys Ile Val Gly Asp Glu Pro Ala Ile Ala
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Pro Cys Gln Ala Ala Leu Trp Gly Met Gly Arg Val Ala Ala Leu Glu
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His Pro Gly Ala Trp Gly Gly Leu Val Asp Leu Asp Pro Arg Ala Ser
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Pro Pro Gln Ala Ser Pro Ile Asp Gly Glu Met Leu Val Thr Glu Leu
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Leu Ser Gln Glu Thr Glu Asp Gln Leu Ala Phe Arg His Gly Arg Arg
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Cys Glu Gln Gln Pro Pro Glu Ile Arg Ala Arg Ile Ala Ala Val Glu
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Ala Asp Val Glu Pro Met Thr Ala Leu Val Ser Ser Val Glu Pro Pro
2725 2730 2735

Leu Arg Gly Val Val His Ala Ala Gly Val Ser Val Met Arg Pro Leu
2740 2745 2750

Ala Glu Thr Asp Glu Thr Leu Leu Glu Ser Val Leu Arg Pro Lys Val
2755 2760 2765

Ala Gly Ser Trp Leu Leu His Arg Leu Leu His Gly Arg Pro Leu Asp
2770 2775 2780

Leu Phe Val Leu Phe Ser Ser Gly Ala Ala Val Trp Gly Ser His Ser
2785 2790 2795 2800

Gln Gly Ala Tyr Ala Ala Ala Asn Ala Phe Leu Asp Gly Leu Ala His

2805 2810 2815

Leu Arg Arg Ser Gln Ser Leu Pro Ala Leu Ser Val Ala Trp Gly Leu
2820 2825 2830

Trp Ala Glu Gly Gly Met Ala Asp Ala Glu Ala His Ala Arg Leu Ser
2835 2840 2845

Asp Ile Gly Val Leu Pro Met Ser Thr Ser Ala Ala Leu Ser Ala Leu
2850 2855 2860

Gln Arg Leu Val Glu Thr Gly Ala Ala Gln Arg Thr Val Thr Arg Met
2865 2870 2875 2880

Asp Trp Ala Arg Phe Ala Pro Val Tyr Thr Ala Arg Gly Arg Arg Asn
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Thr Val Gln Arg Leu Val Glu His Leu Leu Val Asp Val Leu Lys Leu
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Glu Asp Arg Ser Asp Thr Gln His Val Arg Ser Leu Ala Ser Asp Glu
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Ser Pro Thr Gly Val Phe Val Gly Ala Gly Pro Asn Glu Tyr Tyr Thr
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Gln Arg Leu Arg Gly Phe Thr Asp Gly Ala Ala Gly Leu Tyr Gly Gly
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Thr Gly Asn Met Leu Ser Val Thr Ala Gly Arg Leu Ser Phe Phe Leu
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Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Leu Gly Glu Cys
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Phe Val Leu Leu Ser Arg Met Arg Ala Leu Ser Pro Asp Gly Arg Cys
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Lys Thr Phe Ser Ala Asp Ala Asp Gly Tyr Ala Arg Gly Glu Gly Cys
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Ser Ser Gly Leu Thr Val Pro Asn Gly Pro Ala Gln Gln Ala Leu Leu
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Arg Gln Ala Leu Ser Gln Ala Gly Val Ser Pro Val Asp Val Asp Phe
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Val Glu Cys His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Val
3330 3335 3340

Gln Ala Leu Ser Glu Val Tyr Gly Pro Gly Arg Ser Gly Asp Arg Pro
3345 3350 3355 3360

Leu Val Leu Gly Ala Ala Lys Ala Asn Val Ala His Leu Glu Ala Ala
3365 3370 3375

Ser Gly Leu Ala Ser Leu Leu Lys Ala Val Leu Ala Leu Arg His Glu
3380 3385 3390

Gln Ile Pro Ala Gln Pro Glu Leu Gly Glu Leu Asn Pro His Leu Pro
3395 3400 3405

Trp Asn Thr Leu Pro Val Ala Val Pro Arg Lys Ala Val Pro Trp Gly
3410 3415 3420

Arg Gly Ala Arg Pro Arg Arg Ala Gly Val Ser Ala Phe Gly Leu Ser
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Gly Thr Asn Val His Val Val Leu Glu Glu Ala Pro Glu Val Glu Pro
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Lys Ser Ala Ala Ala Leu Asp Ala Ala Ala Ala Arg Leu Ser Ala His
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Leu Ser Ala His Pro Glu Leu Ser Leu Gly Asp Val Ala Phe Ser Leu
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Ala Thr Thr Arg Ser Pro Met Glu His Arg Leu Ala Ile Ala Thr Thr
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Ser Arg Glu Ala Leu Arg Gly Ala Leu Asp Ala Ala Ala Gln Gln Lys
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Thr Pro Gln Gly Ala Val Arg Gly Lys Ala Val Ser Ser Arg Gly Lys
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Cys Val Ala Leu Phe Asp Arg Glu Ile Asp Gln Pro Leu Arg Glu Val
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Met Trp Ala Ala Pro Gly Leu Ala Gln Ala Ala Arg Leu Asp Gln Thr
3605 3610 3615

Ala Tyr Ala Gln Pro Ala Leu Phe Ala Leu Glu Tyr Ala Leu Ala Ala
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Leu Trp Arg Ser Trp Gly Val Glu Pro His Val Leu Leu Gly His Ser
3635 3640 3645

Ile Gly Glu Leu Val Ala Ala Cys Val Ala Gly Val Phe Ser Leu Glu
3650 3655 3660

Asp Ala Val Arg Leu Val Ala Ala Arg Gly Arg Leu Met Gln Ala Leu
3665 3670 3675 3680

Pro Ala Gly Gly Ala Met Val Ala Ile Ala Ala Ser Glu Ala Glu Val
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Ala Ala Ser Val Ala Pro His Ala Ala Thr Val Ser Ile Ala Ala Val
3700 3705 3710

Asn Gly Pro Asp Ala Val Val Ile Ala Gly Ala Glu Val Gln Val Leu
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Ala Leu Gly Ala Thr Phe Ala Ala Arg Gly Ile Arg Thr Lys Arg Leu
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Ala Val Ser His Ala Phe His Ser Pro Leu Met Asp Pro Met Leu Glu
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Asp Phe Gln Arg Val Ala Ala Thr Ile Ala Tyr Arg Ala Pro Asp Arg
3765 3770 3775

Pro Val Val Ser Asn Val Thr Gly His Val Ala Gly Pro Glu Ile Ala
3780 3785 3790

Thr Pro Glu Tyr Trp Val Arg His Val Arg Ser Ala Val Arg Phe Gly
3795 3800 3805

Asp Gly Ala Lys Ala Leu His Ala Ala Gly Ala Ala Thr Phe Val Glu
3810 3815 3820

Val Gly Pro Lys Pro Val Leu Leu Gly Leu Leu Pro Ala Cys Leu Gly
3825 3830 3835 3840

Glu Ala Asp Ala Val Leu Val Pro Ser Leu Arg Ala Asp Arg Ser Glu

3845 3850 3855

Cys Glu Val Val Leu Ala Ala Leu Gly Ala Trp Tyr Ala Trp Gly Gly
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Ala Leu Asp Trp Lys Gly Val Phe Pro Asp Gly Ala Arg Arg Val Ala
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Leu Pro Met Tyr Pro Trp Gln Arg Glu Arg His Trp Met Asp Leu Thr
3890 3895 3900

Pro Arg Ser Ala Ala Pro Ala Gly Ile Ala Gly Arg Trp Pro Leu Ala
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Gly Val Gly Leu Cys Met Pro Gly Ala Val Leu His His Val Leu Ser
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Ile Gly Pro Arg His Gln Pro Phe Leu Gly Asp His Leu Val Phe Gly
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Lys Val Val Val Pro Gly Ala Phe His Val Ala Val Ile Leu Ser Ile
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Ala Ala Glu Arg Trp Pro Glu Arg Ala Ile Glu Leu Thr Gly Val Glu
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Arg Gly Arg Val Gln Pro Thr Asp Gly Ala Pro Gly Ala Leu Pro Arg
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Met Ala Ala Ala Leu Ala Thr Arg Leu Asn Arg Cys Val Leu Ala Glu
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Pro Lys Gly Leu Glu Ala Ala Leu Ala Gly Val Ser Pro Ala Gly Val
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Ile Cys Leu Trp Glu Ala Gly Ala His Glu Glu Ala Pro Ala Ala Ala
4275 4280 4285

Gln Arg Val Ala Thr Glu Gly Leu Ser Val Val Gln Ala Leu Arg Asp
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Arg Ala Val Arg Leu Trp Trp Val Thr Met Gly Ala Val Ala Val Glu
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Glu Leu Gly Arg Ala Asp Asp Glu Thr Gln Val Ala Phe Arg Ser Gly
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Lys Arg Arg Val Ala Arg Leu Val Lys Ala Thr Thr Pro Glu Gly Leu
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Thr Leu Asp Gln Leu Arg Leu Ala Pro Ala Gln Arg Arg Ala Pro Gly
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Pro Gly Glu Val Glu Ile Lys Val Thr Ala Ser Gly Leu Asn Phe Arg
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Thr Val Leu Ala Val Leu Gly Met Tyr Pro Gly Asp Ala Gly Pro Met
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Gly Gly Asp Cys Ala Gly Val Ala Thr Ala Val Gly Gln Gly Val Arg
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His Val Ala Val Gly Asp Ala Val Met Thr Leu Gly Thr Leu His Arg
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Thr Pro Ala Gln Ala Ala Thr Val Pro Val Ala Phe Leu Thr Ala Trp
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Ser Leu Ser Leu Leu Ser Thr Gly Gly Arg Phe Leu Glu Met Gly Lys
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Thr Asp Ile Arg Asp Arg Ala Ala Val Ala Ala Ala His Pro Gly Val
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Arg Tyr Arg Val Phe Asp Ile Leu Glu Leu Ala Pro Asp Arg Thr Arg
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Glu Ile Leu Glu Arg Val Val Glu Gly Phe Ala Ala Gly His Leu Arg
4675 4680 4685

Ala Leu Pro Val His Ala Phe Ala Ile Thr Lys Ala Glu Ala Ala Phe
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Ala Pro Ser Ala Ala Pro Leu Ala Pro Thr Gly Thr Val Leu Leu Thr
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Gln Gly Val Pro His Met Val Leu Thr Gly Arg Arg Gly Leu Asp Thr
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Val Thr Ile Ala Ala Ser Asp Val Ala Asp Arg Asn Ala Leu Glu Ala
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Arg Phe Ser Arg Val Leu Ala Pro Lys Val Thr Gly Ala Trp Asn Leu
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His Glu Leu Thr Ala Gly Asn Asp Leu Ala Phe Phe Val Leu Phe Ser
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Ser Met Ser Gly Leu Leu Gly Ser Ala Gly Gln Ser Asn Tyr Ala Ala
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Ala Asn Thr Phe Leu Asp Ala Leu Ala Ala His Arg Arg Ala Glu Gly

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Ser Val Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala
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Gly Val Ile Lys Val Ala Leu Ala Leu Glu Arg Gly Leu Ile Pro Arg
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Ser Leu His Phe Asp Ala Pro Asn Pro His Ile Pro Trp Ser Glu Leu
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Ala Val Gln Val Ala Ala Lys Pro Val Glu Trp Thr Arg Asn Gly Val
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Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser Gly Thr Asn Ala
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His Val Val Leu Glu Glu Ala Pro Ala Ala Ala Phe Ala Pro Ala Ala
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Ala Arg Ser Ala Glu Leu Phe Val Leu Ser Ala Lys Ser Ala Ala Ala
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Leu Asp Ala Gln Ala Ala Arg Leu Ser Ala His Val Val Ala His Pro
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Glu Leu Gly Leu Gly Asp Leu Ala Phe Ser Leu Ala Thr Thr Arg Ser
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His Ala Ala Gly Ile Leu Asp Asp Gly Leu Leu Met Gln Gln Thr Pro
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<212> PRT
<213> Sorangium cellulosum

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Gly Ala Gly Thr Pro Glu Ala Phe Trp Glu Leu Leu Asp Asp Gly Arg
50 55 60

Asp Ala Ile Arg Pro Leu Glu Glu Arg Trp Ala Leu Val Gly Val Asp
65 70 75 80

Pro Gly Asp Asp Val Pro Arg Trp Ala Gly Leu Leu Thr Glu Ala Ile
85 90 95

Asp Gly Phe Asp Ala Ala Phe Phe Gly Ile Ala Pro Arg Glu Ala Arg
100 105 110

Ser Leu Asp Pro Gln His Arg Leu Leu Leu Glu Val Ala Trp Glu Gly
115 120 125

Phe Glu Asp Ala Gly Ile Pro Pro Arg Ser Leu Val Gly Ser Arg Thr
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Gly Val Phe Val Gly Val Cys Ala Thr Glu Tyr Leu His Ala Ala Val
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Ala His Gln Pro Arg Glu Glu Arg Asp Ala Tyr Ser Thr Thr Gly Asn
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Met Leu Ser Ile Ala Ala Gly Arg Leu Ser Tyr Thr Leu Gly Leu Gln
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Gly Pro Cys Leu Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala
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Ile His Leu Ala Cys Arg Ser Leu Arg Ala Arg Glu Ser Asp Leu Ala
210 215 220

Leu Ala Gly Gly Val Asn Met Leu Leu Ser Pro Asp Thr Met Arg Ala
225 230 235 240

Leu Ala Arg Thr Gln Ala Leu Ser Pro Asn Gly Arg Cys Gln Thr Phe
245 250 255

Asp Ala Ser Ala Asn Gly Phe Val Arg Gly Glu Gly Cys Gly Leu Ile
260 265 270

Val Leu Lys Arg Leu Ser Asp Ala Arg Arg Asp Gly Asp Arg Ile Trp
275 280 285

Ala Leu Ile Arg Gly Ser Ala Ile Asn Gln Asp Gly Arg Ser Thr Gly
290 295 300

Leu Thr Ala Pro Asn Val Leu Ala Gln Gly Ala Leu Leu Arg Glu Ala
305 310 315 320

Leu Arg Asn Ala Gly Val Glu Ala Glu Ala Ile Gly Tyr Ile Glu Thr
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His Gly Ala Ala Thr Ser Leu Gly Asp Pro Ile Glu Ile Glu Ala Leu
340 345 350

Arg Ala Val Val Gly Pro Ala Arg Ala Asp Gly Ala Arg Cys Val Leu

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Arg Asn Leu Asn Phe Arg Thr Leu Asn Pro Arg Ile Arg Ile Glu Gly
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Thr Ala Leu Ala Leu Ala Thr Glu Pro Val Pro Trp Pro Arg Thr Gly
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Arg Thr Arg Phe Ala Gly Val Ser Ser Phe Gly Met Ser Gly Thr Asn
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Ala His Val Val Leu Glu Glu Ala Pro Ala Val Glu Pro Glu Ala Ala
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Ala Pro Glu Arg Ala Ala Glu Leu Phe Val Leu Ser Ala Lys Ser Ala
465                 470                 475                 480

Ala Ala Leu Asp Ala Gln Ala Ala Arg Leu Arg Asp His Leu Glu Lys
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His Val Glu Leu Gly Leu Gly Asp Val Ala Phe Ser Leu Ala Thr Thr
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Arg Ser Ala Met Glu His Arg Leu Ala Val Ala Ala Ser Ser Arg Glu
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Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Val Gly Met Gly Arg Lys
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Arg Ala Ile Glu Ala Glu Ala Gly Trp Ser Leu Leu Gly Glu Leu Ser
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Val Leu Phe Ala Met Glu Val Ala Leu Ser Ala Leu Trp Arg Ser Trp
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Gly Val Glu Pro Glu Ala Val Val Gly His Ser Met Gly Glu Val Ala
                645                 650                 655

Ala Ala His Val Ala Gly Ala Leu Ser Leu Glu Asp Ala Val Ala Ile
            660                 665                 670

Ile Cys Arg Arg Ser Arg Leu Leu Arg Arg Ile Ser Gly Gln Gly Glu
        675                 680                 685

Met Ala Leu Val Glu Leu Ser Leu Glu Glu Ala Glu Ala Ala Leu Arg
    690                 695                 700
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Gly His Glu Gly Arg Leu Ser Val Ala Val Ser Asn Ser Pro Arg Ser
705 710 715 720

Thr Val Leu Ala Gly Glu Pro Ala Ala Leu Ser Glu Val Leu Ala Ala
725 730 735

Leu Thr Ala Lys Gly Val Phe Trp Arg Gln Val Lys Val Asp Val Ala
740 745 750

Ser His Ser Pro Gln Val Asp Pro Leu Arg Glu Glu Leu Ile Ala Ala
755 760 765

Leu Gly Ala Ile Arg Pro Arg Ala Ala Ala Val Pro Met Arg Ser Thr
770 775 780

Val Thr Gly Gly Val Ile Ala Gly Pro Glu Leu Gly Ala Ser Tyr Trp
785 790 795 800

Ala Asp Asn Leu Arg Gln Pro Val Arg Phe Ala Ala Ala Ala Gln Ala
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Leu Leu Glu Gly Gly Pro Ala Leu Phe Ile Glu Met Ser Pro His Pro
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Ile Leu Val Pro Pro Leu Asp Glu Ile Gln Thr Ala Ala Glu Gln Gly
835 840 845

Gly Ala Ala Val Gly Ser Leu Arg Arg Gly Gln Asp Glu Arg Ala Thr
850 855 860

Leu Leu Glu Ala Leu Gly Thr Leu Trp Ala Ser Gly Tyr Pro Val Ser
865 870 875 880

Trp Ala Arg Leu Phe Pro Ala Gly Gly Arg Arg Val Pro Leu Pro Thr
885 890 895

Tyr Pro Trp Gln His Glu Arg Cys Trp Ile Glu Val Glu Pro Asp Ala
900 905 910

Arg Arg Leu Ala Ala Ala Asp Pro Thr Lys Asp Trp Phe Tyr Arg Thr
915 920 925

Asp Trp Pro Glu Val Pro Arg Ala Ala Pro Lys Ser Glu Thr Ala His
930 935 940

Gly Ser Trp Leu Leu Leu Ala Asp Arg Gly Gly Val Gly Glu Ala Val
945 950 955 960

Ala Ala Ala Leu Ser Thr Arg Gly Leu Ser Cys Thr Val Leu His Ala
965 970 975

Ser Ala Asp Ala Ser Thr Val Ala Glu Gln Val Ser Glu Ala Ala Ser
980 985 990

Arg Arg Asn Asp Trp Gln Gly Val Leu Tyr Leu Trp Gly Leu Asp Ala
995 1000 1005

Val Val Asp Ala Gly Ala Ser Ala Asp Glu Val Ser Glu Ala Thr Arg
1010 1015 1020

Arg Ala Thr Ala Pro Val Leu Gly Leu Val Arg Phe Leu Ser Ala Ala
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Pro His Pro Pro Arg Phe Trp Val Val Thr Arg Gly Ala Cys Thr Val
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Gly Gly Glu Pro Glu Ala Ser Leu Cys Gln Ala Ala Leu Trp Gly Leu
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Ala Arg Val Ala Ala Leu Glu His Pro Ala Ala Trp Gly Gly Leu Val
1075 1080 1085

Asp Leu Asp Pro Gln Lys Ser Pro Thr Glu Ile Glu Pro Leu Val Ala
1090 1095 1100

Glu Leu Leu Ser Pro Asp Ala Glu Asp Gln Leu Ala Phe Arg Ser Gly
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Arg Arg His Ala Ala Arg Leu Val Ala Ala Pro Pro Glu Gly Asp Val
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Ala Pro Ile Ser Leu Ser Ala Glu Gly Ser Tyr Leu Val Thr Gly Gly
1140 1145 1150

Leu Gly Gly Leu Gly Leu Leu Val Ala Arg Trp Leu Val Glu Arg Gly
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Ala Arg His Leu Val Leu Thr Ser Arg His Gly Leu Pro Glu Arg Gln
1170 1175 1180

Ala Ser Gly Gly Glu Gln Pro Pro Glu Ala Arg Ala Arg Ile Ala Ala
1185 1190 1195 1200

Val Glu Gly Leu Glu Ala Gln Gly Ala Arg Val Thr Val Ala Ala Val
1205 1210 1215

Asp Val Ala Glu Ala Asp Pro Met Thr Ala Leu Leu Ala Ala Ile Glu
1220 1225 1230

Pro Pro Leu Arg Gly Val Val His Ala Ala Gly Val Phe Pro Val Arg
1235 1240 1245

His Leu Ala Glu Thr Asp Glu Ala Leu Leu Glu Ser Val Leu Arg Pro
1250 1255 1260

Lys Val Ala Gly Ser Trp Leu Leu His Arg Leu Leu Arg Asp Arg Pro
1265 1270 1275 1280

Leu Asp Leu Phe Val Leu Phe Ser Ser Gly Ala Ala Val Trp Gly Gly
1285 1290 1295

Lys Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Phe Leu Asp Gly Leu
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Ala His His Arg Arg Ala His Ser Leu Pro Ala Leu Ser Leu Ala Trp
1315 1320 1325

Gly Leu Trp Ala Glu Gly Gly Met Val Asp Ala Lys Ala His Ala Arg
1330 1335 1340

Leu Ser Asp Ile Gly Val Leu Pro Met Ala Thr Gly Pro Ala Leu Ser
1345 1350 1355 1360

Ala Leu Glu Arg Leu Val Asn Thr Ser Ala Val Gln Arg Ser Val Thr
1365 1370 1375

Arg Met Asp Trp Ala Arg Phe Ala Pro Val Tyr Ala Ala Arg Gly Arg
1380 1385 1390

Arg Asn Leu Leu Ser Ala Leu Val Ala Glu Asp Glu Arg Ala Ala Ser

1395 1400 1405

Pro Pro Val Pro Thr Ala Asn Arg Ile Trp Arg Gly Leu Ser Val Ala
1410 1415 1420

Glu Ser Arg Ser Ala Leu Tyr Glu Leu Val Arg Gly Ile Val Ala Arg
1425 1430 1435 1440

Val Leu Gly Phe Ser Asp Pro Gly Ala Leu Asp Val Gly Arg Gly Phe
1445 1450 1455

Ala Glu Gln Gly Leu Asp Ser Leu Met Ala Leu Glu Ile Arg Asn Arg
1460 1465 1470

Leu Gln Arg Glu Leu Gly Glu Arg Leu Ser Ala Thr Leu Ala Phe Asp
1475 1480 1485

His Pro Thr Val Glu Arg Leu Val Ala His Leu Leu Thr Asp Val Leu
1490 1495 1500

Lys Leu Glu Asp Arg Ser Asp Thr Arg His Ile Arg Ser Val Ala Ala
1505 1510 1515 1520

Asp Asp Asp Ile Ala Ile Val Gly Ala Ala Cys Arg Phe Pro Gly Gly
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Asp Glu Gly Leu Glu Thr Tyr Trp Arg His Leu Ala Glu Gly Met Val
1540 1545 1550

Val Ser Thr Glu Val Pro Ala Asp Arg Trp Arg Ala Ala Asp Trp Tyr
1555 1560 1565

Asp Pro Asp Pro Glu Val Pro Gly Arg Thr Tyr Val Ala Lys Gly Ala
1570 1575 1580

Phe Leu Arg Asp Val Arg Ser Leu Asp Ala Ala Phe Phe Ala Ile Ser
1585 1590 1595 1600

Pro Arg Glu Ala Met Ser Leu Asp Pro Gln Gln Arg Leu Leu Leu Glu
1605 1610 1615

Val Ser Trp Glu Ala Ile Glu Arg Ala Gly Gln Asp Pro Met Ala Leu
1620 1625 1630

Arg Glu Ser Ala Thr Gly Val Phe Val Gly Met Ile Gly Ser Glu His
1635 1640 1645

Ala Glu Arg Val Gln Gly Leu Asp Asp Asp Ala Ala Leu Leu Tyr Gly
1650 1655 1660

Thr Thr Gly Asn Leu Leu Ser Val Ala Ala Gly Arg Leu Ser Phe Phe
1665 1670 1675 1680

Leu Gly Leu His Gly Pro Thr Met Thr Val Asp Thr Ala Cys Ser Ser
1685 1690 1695

Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Leu Gly Glu
1700 1705 1710

Cys Asp Gln Ala Leu Ala Gly Gly Ser Ser Val Leu Leu Ser Pro Arg
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Ser Phe Val Ala Ala Ser Arg Met Arg Leu Leu Ser Pro Asp Gly Arg
1730 1735 1740

Cys Lys Thr Phe Ser Ala Ala Ala Asp Gly Phe Ala Arg Ala Glu Gly
1745 1750 1755 1760

Cys Ala Val Val Val Leu Lys Arg Leu Arg Asp Ala Gln Arg Asp Arg
1765 1770 1775

Asp Pro Ile Leu Ala Val Val Arg Ser Thr Ala Ile Asn His Asp Gly
1780 1785 1790

Pro Ser Ser Gly Leu Thr Val Pro Ser Gly Pro Ala Gln Gln Ala Leu
1795 1800 1805

Leu Arg Gln Ala Leu Ala Gln Ala Gly Val Ala Pro Ala Glu Val Asp
1810 1815 1820

Phe Val Glu Cys His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu
1825 1830 1835 1840

Val Gln Ala Leu Gly Ala Val Tyr Gly Arg Gly Arg Pro Ala Glu Arg
1845 1850 1855

Pro Leu Trp Leu Gly Ala Val Lys Ala Asn Leu Gly His Leu Glu Ala
1860 1865 1870

Ala Ala Gly Leu Ala Gly Val Leu Lys Val Leu Leu Ala Leu Glu His
1875 1880 1885

Glu Gln Ile Pro Ala Gln Pro Glu Leu Asp Glu Leu Asn Pro His Ile
1890 1895 1900

Pro Trp Ala Glu Leu Pro Val Ala Val Val Arg Arg Ala Val Pro Trp
1905 1910 1915 1920

Pro Arg Gly Ala Arg Pro Arg Arg Ala Gly Val Ser Ala Phe Gly Leu
1925 1930 1935

Ser Gly Thr Asn Ala His Val Val Leu Glu Glu Ala Pro Ala Val Glu
1940 1945 1950

Pro Val Ala Ala Ala Pro Glu Arg Ala Ala Glu Leu Phe Val Leu Ser
1955 1960 1965

Ala Lys Ser Ala Ala Ala Leu Asp Ala Gln Ala Ala Arg Leu Arg Asp
1970 1975 1980

His Leu Glu Lys His Val Glu Leu Gly Leu Gly Asp Val Ala Phe Ser
1985 1990 1995 2000

Leu Ala Thr Thr Arg Ser Ala Met Glu His Arg Leu Ala Val Ala Ala
2005 2010 2015

Ser Ser Arg Glu Ala Leu Arg Gly Ala Leu Ser Ala Ala Ala Gln Gly
2020 2025 2030

His Thr Pro Pro Gly Ala Val Arg Gly Arg Ala Ser Gly Gly Ser Ala
2035 2040 2045

Pro Lys Val Val Phe Val Phe Pro Gly Gln Gly Ser Gln Trp Val Gly
2050 2055 2060

Met Gly Arg Lys Leu Met Ala Glu Glu Pro Val Phe Arg Ala Ala Leu
2065 2070 2075 2080

Glu Gly Cys Asp Arg Ala Ile Glu Ala Glu Ala Gly Trp Ser Leu Leu
2085 2090 2095

Gly Glu Leu Ser Ala Asp Glu Ala Ala Ser Gln Leu Gly Arg Ile Asp
2100 2105 2110

Val Val Gln Pro Val Leu Phe Ala Met Glu Val Ala Leu Ser Ala Leu
2115 2120 2125

Trp Arg Ser Trp Gly Val Glu Pro Glu Ala Val Val Gly His Ser Met
2130 2135 2140

Gly Glu Val Ala Ala Ala His Val Ala Gly Ala Leu Ser Leu Glu Asp
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Ala Val Ala Ile Ile Cys Arg Arg Ser Arg Leu Leu Arg Arg Ile Ser
2165 2170 2175

Gly Gln Gly Glu Met Ala Leu Val Glu Leu Ser Leu Glu Glu Ala Glu
2180 2185 2190

Ala Ala Leu Arg Gly His Glu Gly Arg Leu Ser Val Ala Val Ser Asn
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Ser Pro Arg Ser Thr Val Leu Ala Gly Glu Pro Ala Ala Leu Ser Glu
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Val Leu Ala Ala Leu Thr Ala Lys Gly Val Phe Trp Arg Gln Val Lys
2225 2230 2235 2240

Val Asp Val Ala Ser His Ser Pro Gln Val Asp Pro Leu Arg Glu Glu
2245 2250 2255

Leu Ile Ala Ala Leu Gly Ala Ile Arg Pro Arg Ala Ala Ala Val Pro
2260 2265 2270

Met Arg Ser Thr Val Thr Gly Gly Val Ile Ala Gly Pro Glu Leu Gly
2275 2280 2285

Ala Ser Tyr Trp Ala Asp Asn Leu Arg Gln Pro Val Arg Phe Ala Ala
2290 2295 2300

Ala Ala Gln Ala Leu Leu Glu Gly Gly Pro Ala Leu Phe Ile Glu Met
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Ser Pro His Pro Ile Leu Val Pro Pro Leu Asp Glu Ile Gln Thr Ala
2325 2330 2335

Ala Glu Gln Gly Gly Ala Ala Val Gly Ser Leu Arg Arg Gly Gln Asp
2340 2345 2350

Glu Arg Ala Thr Leu Leu Glu Ala Leu Gly Thr Leu Trp Ala Ser Gly
2355 2360 2365

Tyr Pro Val Ser Trp Ala Arg Leu Phe Pro Ala Gly Gly Arg Arg Val
2370 2375 2380

Pro Leu Pro Thr Tyr Pro Trp Gln His Glu Arg Tyr Trp Ile Glu Asp
2385 2390 2395 2400

Ser Val His Gly Ser Lys Pro Ser Leu Arg Leu Arg Gln Leu Arg Asn
2405 2410 2415

Gly Ala Thr Asp His Pro Leu Leu Gly Ala Pro Leu Leu Val Ser Ala
2420 2425 2430

Arg Pro Gly Ala His Leu Trp Glu Gln Ala Leu Ser Asp Glu Arg Leu

2435 2440 2445

Ser Tyr Leu Ser Glu His Arg Val His Gly Glu Ala Val Leu Pro Ser
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Ala Ala Tyr Val Glu Met Ala Leu Ala Ala Gly Val Asp Leu Tyr Gly
2465 2470 2475 2480

Thr Ala Thr Leu Val Leu Glu Gln Leu Ala Leu Glu Arg Ala Leu Ala
2485 2490 2495

Val Pro Ser Glu Gly Gly Arg Ile Val Gln Val Ala Leu Ser Glu Glu
2500 2505 2510

Gly Pro Gly Arg Ala Ser Phe Gln Val Ser Ser Arg Glu Glu Ala Gly
2515 2520 2525

Arg Ser Trp Val Arg His Ala Thr Gly His Val Cys Ser Gly Gln Ser
2530 2535 2540

Ser Ala Val Gly Ala Leu Lys Glu Ala Pro Trp Glu Ile Gln Arg Arg
2545 2550 2555 2560

Cys Pro Ser Val Leu Ser Ser Glu Ala Leu Tyr Pro Leu Leu Asn Glu
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His Ala Leu Asp Tyr Gly Pro Cys Phe Gln Gly Val Glu Gln Val Trp
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Leu Gly Thr Gly Glu Val Leu Gly Arg Val Arg Leu Pro Gly Asp Met
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Ala Ser Ser Ser Gly Ala Tyr Arg Ile His Pro Ala Leu Leu Asp Ala
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Cys Phe Gln Val Leu Thr Ala Leu Leu Thr Thr Pro Glu Ser Ile Glu
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Ile Arg Arg Arg Leu Thr Asp Leu His Glu Pro Asp Leu Pro Arg Ser
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Arg Ala Pro Val Asn Gln Ala Val Ser Asp Thr Trp Leu Trp Asp Ala
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Ala Leu Asp Gly Gly Arg Arg Gln Ser Ala Ser Val Pro Val Asp Leu
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Val Leu Gly Ser Phe His Ala Lys Trp Glu Val Met Glu Arg Leu Ala
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Gln Ala Tyr Ile Ile Gly Thr Leu Arg Ile Trp Asn Val Phe Cys Ala
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Ala Gly Glu Arg His Thr Ile Asp Glu Leu Leu Val Arg Leu Gln Ile
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Ser Val Val Tyr Arg Lys Val Ile Lys Arg Trp Met Glu His Leu Val
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Ala Ile Gly Ile Leu Val Gly Asp Gly Glu His Phe Val Ser Ser Gln
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Pro Leu Pro Glu Pro Asp Leu Ala Ala Val Leu Glu Glu Ala Gly Arg
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Val Phe Ala Asp Leu Pro Val Leu Phe Glu Trp Cys Lys Phe Ala Gly
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Glu Arg Leu Ala Asp Val Leu Thr Gly Lys Thr Leu Ala Leu Glu Ile
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Leu Phe Pro Gly Gly Ser Phe Asp Met Ala Glu Arg Ile Tyr Arg Asp
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Ser Pro Ile Ala Arg Tyr Ser Asn Gly Ile Val Arg Gly Val Val Glu
2835 2840 2845

Ser Ala Ala Arg Val Val Ala Pro Ser Gly Met Phe Ser Ile Leu Glu
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Ile Gly Ala Gly Thr Gly Ala Thr Thr Ala Ala Val Leu Pro Val Leu
2865 2870 2875 2880

Leu Pro Asp Arg Thr Glu Tyr His Phe Thr Asp Val Ser Pro Leu Phe
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Leu Ala Arg Ala Glu Gln Arg Phe Arg Asp Tyr Pro Phe Leu Lys Tyr
2900 2905 2910

Gly Ile Leu Asp Val Asp Gln Glu Pro Ala Gly Gln Gly Tyr Ala His
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Gln Arg Phe Asp Val Ile Val Ala Ala Asn Val Ile His Ala Thr Arg
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Asp Ile Arg Ala Thr Ala Lys Arg Leu Leu Ser Leu Leu Ala Pro Gly
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Gly Leu Leu Val Leu Val Glu Gly Thr Gly His Pro Ile Trp Phe Asp
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Ile Thr Thr Gly Leu Ile Glu Gly Trp Gln Lys Tyr Glu Asp Asp Leu
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Arg Ile Asp His Pro Leu Leu Pro Ala Arg Thr Trp Cys Asp Val Leu
2995 3000 3005

Arg Arg Val Gly Phe Ala Asp Ala Val Ser Leu Pro Gly Asp Gly Ser
3010 3015 3020

Pro Ala Gly Ile Leu Gly Gln His Val Ile Leu Ser Arg Ala Pro Gly
3025 3030 3035 3040

Ile Ala Gly Ala Ala Cys Asp Ser Ser Gly Glu Ser Ala Thr Glu Ser
3045 3050 3055

Pro Ala Ala Arg Ala Val Arg Gln Glu Trp Ala Asp Gly Ser Ala Asp
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Val Val His Arg Met Ala Leu Glu Arg Met Tyr Phe His Arg Arg Pro
3075 3080 3085

Gly Arg Gln Val Trp Val His Gly Arg Leu Arg Thr Gly Gly Gly Ala
3090 3095 3100

Phe Thr Lys Ala Leu Ala Gly Asp Leu Leu Leu Phe Glu Asp Thr Gly
3105 3110 3115 3120

Gln Val Val Ala Glu Val Gln Gly Leu Arg Leu Pro Gln Leu Glu Ala
3125 3130 3135

Ser Ala Phe Ala Pro Arg Asp Pro Arg Glu Glu Trp Leu Tyr Ala Leu
3140 3145 3150

Glu Trp Gln Arg Lys Asp Pro Ile Pro Glu Ala Pro Ala Ala Ala Ser
3155 3160 3165

Ser Ser Ser Ala Gly Ala Trp Leu Val Leu Met Asp Gln Gly Gly Thr
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Gly Ala Ala Leu Val Ser Leu Leu Glu Gly Arg Gly Glu Ala Cys Val
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Arg Val Ile Ala Gly Thr Ala Tyr Ala Cys Leu Ala Pro Gly Leu Tyr
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Gln Val Asp Pro Ala Gln Pro Asp Gly Phe His Thr Leu Leu Arg Asp
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Ala Phe Gly Glu Asp Arg Ile Cys Arg Ala Val Val His Met Trp Ser
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Leu Asp Ala Thr Ala Ala Gly Glu Arg Ala Thr Ala Glu Ser Leu Gln
3250 3255 3260

Ala Asp Gln Leu Leu Gly Ser Leu Ser Ala Leu Ser Leu Val Gln Ala
3265 3270 3275 3280

Leu Val Arg Arg Arg Trp Arg Asn Met Pro Arg Leu Trp Leu Leu Thr
3285 3290 3295

Arg Ala Val His Ala Val Gly Ala Glu Asp Ala Ala Ala Ser Val Ala
3300 3305 3310

Gln Ala Pro Val Trp Gly Leu Gly Arg Thr Leu Ala Leu Glu His Pro
3315 3320 3325

Glu Leu Arg Cys Thr Leu Val Asp Val Asn Pro Ala Pro Ser Pro Glu
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Asp Ala Ala Ala Leu Ala Val Glu Leu Gly Ala Ser Asp Arg Glu Asp
3345 3350 3355 3360

Gln Val Ala Leu Arg Ser Asp Gly Arg Tyr Val Ala Arg Leu Val Arg
3365 3370 3375

Ser Ser Phe Ser Gly Lys Pro Ala Thr Asp Cys Gly Ile Arg Ala Asp
3380 3385 3390

Gly Ser Tyr Val Ile Thr Asp Gly Met Gly Arg Val Gly Leu Ser Val
3395 3400 3405

Ala Gln Trp Met Val Met Gln Gly Ala Arg His Val Val Leu Val Asp
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Arg Gly Gly Ala Ser Glu Ala Ser Arg Asp Ala Leu Arg Ser Met Ala
3425 3430 3435 3440

Glu Ala Gly Ala Glu Val Gln Ile Val Glu Ala Asp Val Ala Arg Arg
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Asp Asp Val Ala Arg Leu Leu Ser Lys Ile Glu Pro Ser Met Pro Pro
3460 3465 3470

Leu Arg Gly Ile Val Tyr Val Asp Gly Thr Phe Gln Gly Asp Ser Ser

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Met Leu Glu Leu Asp Ala Arg Arg Phe Lys Glu Trp Met Tyr Pro Lys
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Val Leu Gly Ala Trp Asn Leu His Ala Leu Thr Arg Asp Arg Ser Leu
3505                3510                3515                3520

Asp Phe Phe Val Leu Tyr Ser Ser Gly Thr Ser Leu Leu Gly Leu Pro
                3525                3530                3535

Gly Gln Gly Ser Arg Ala Ala Gly Asp Ala Phe Leu Asp Ala Ile Ala
            3540                3545                3550

His His Arg Cys Lys Val Gly Leu Thr Ala Met Ser Ile Asn Trp Gly
        3555                3560                3565

Leu Leu Ser Glu Ala Ser Ser Pro Ala Thr Pro Asn Asp Gly Gly Ala
   3570                3575                3580

Arg Leu Glu Tyr Arg Gly Met Glu Gly Leu Thr Leu Glu Gln Gly Ala
3585                3590                3595                3600

Ala Ala Leu Gly Arg Leu Leu Ala Arg Pro Arg Ala Gln Val Gly Val
                3605                3610                3615

Met Arg Leu Asn Leu Arg Gln Trp Leu Glu Phe Tyr Pro Asn Ala Ala
            3620                3625                3630

Arg Leu Ala Leu Trp Ala Glu Leu Leu Lys Glu Arg Asp Arg Ala Asp
        3635                3640                3645

Arg Gly Ala Ser Asn Ala Ser Asn Leu Arg Glu Ala Leu Gln Ser Ala
   3650                3655                3660

Arg Pro Glu Asp Arg Gln Leu Ile Leu Glu Lys His Leu Ser Glu Leu
3665                3670                3675                3680

Leu Gly Arg Gly Leu Arg Leu Pro Pro Glu Arg Ile Glu Arg His Val
                3685                3690                3695

Pro Phe Ser Asn Leu Gly Met Asp Ser Leu Ile Gly Leu Glu Leu Arg
            3700                3705                3710

Asn Arg Ile Glu Ala Ala Leu Gly Ile Thr Val Pro Ala Thr Leu Leu
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Trp Thr Tyr Pro Asn Val Ala Ala Leu Ser Gly Ser Leu Leu Asp Ile
   3730                3735                3740

Leu Phe Pro Asn Ala Gly Ala Thr His Ala Pro Ala Thr Glu Arg Glu
3745                3750                3755                3760

Lys Ser Phe Glu Asn Asp Ala Ala Asp Leu Glu Ala Leu Arg Gly Met
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Thr Asp Glu Gln Lys Asp Ala Leu Leu Ala Glu Lys Leu Ala Gln Leu
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Ala Gln Ile Val Gly Glu
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<211> 2439

<212> PRT
<213> Sorangium cellulosum

<400> 7

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            20                  25                  30

Pro Ile Ala Ile Val Gly Ile Gly Cys Arg Phe Pro Gly Gly Ala Asp
        35                  40                  45

Thr Pro Glu Ala Phe Trp Glu Leu Leu Asp Ser Gly Arg Asp Ala Val
    50                  55                  60

Gln Pro Leu Asp Arg Arg Trp Ala Leu Val Gly Val His Pro Ser Glu
65                  70                  75                  80

Glu Val Pro Arg Trp Ala Gly Leu Leu Thr Glu Ala Val Asp Gly Phe
                85                  90                  95

Asp Ala Ala Phe Phe Gly Thr Ser Pro Arg Glu Ala Arg Ser Leu Asp
            100                 105                 110

Pro Gln Gln Arg Leu Leu Leu Glu Val Thr Trp Glu Gly Leu Glu Asp
        115                 120                 125

Ala Gly Ile Ala Pro Gln Ser Leu Asp Gly Ser Arg Thr Gly Val Phe
    130                 135                 140

Leu Gly Ala Cys Ser Ser Asp Tyr Ser His Thr Val Ala Gln Gln Arg
145                 150                 155                 160

Arg Glu Glu Gln Asp Ala Tyr Asp Ile Thr Gly Asn Thr Leu Ser Val
                165                 170                 175

Ala Ala Gly Arg Leu Ser Tyr Thr Leu Gly Leu Gln Gly Pro Cys Leu
            180                 185                 190

Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Ile His Leu Ala
        195                 200                 205

Cys Arg Ser Leu Arg Ala Arg Glu Ser Asp Leu Ala Leu Ala Gly Gly
    210                 215                 220

Val Asn Met Leu Leu Ser Ser Lys Thr Met Ile Met Leu Gly Arg Ile
225                 230                 235                 240

Gln Ala Leu Ser Pro Asp Gly His Cys Arg Thr Phe Asp Ala Ser Ala
                245                 250                 255

Asn Gly Phe Val Arg Gly Glu Gly Cys Gly Met Val Val Leu Lys Arg
            260                 265                 270

Leu Ser Asp Ala Gln Arg His Gly Asp Arg Ile Trp Ala Leu Ile Arg
        275                 280                 285

Gly Ser Ala Met Asn Gln Asp Gly Arg Ser Thr Gly Leu Met Ala Pro
    290                 295                 300

Asn Val Leu Ala Gln Glu Ala Leu Leu Arg Glu Ala Leu Gln Ser Ala
305                 310                 315                 320

Arg Val Asp Ala Gly Ala Ile Gly Tyr Val Glu Thr His Gly Thr Gly
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325 330 335

Thr Ser Leu Gly Asp Pro Ile Glu Val Glu Ala Leu Arg Ala Val Leu
340 345 350

Gly Pro Ala Arg Ala Asp Gly Ser Arg Cys Val Leu Gly Ala Val Lys
355 360 365

Thr Asn Leu Gly His Leu Glu Gly Ala Ala Gly Val Ala Gly Leu Ile
370 375 380

Lys Ala Ala Leu Ala Leu His His Glu Leu Ile Pro Arg Asn Leu His
385 390 395 400

Phe His Thr Leu Asn Pro Arg Ile Arg Ile Glu Gly Thr Ala Leu Ala
405 410 415

Leu Ala Thr Glu Pro Val Pro Trp Pro Arg Ala Gly Arg Pro Arg Phe
420 425 430

Ala Gly Val Ser Ala Phe Gly Leu Ser Gly Thr Asn Val His Val Val
435 440 445

Leu Glu Glu Ala Pro Ala Thr Val Leu Ala Pro Ala Thr Pro Gly Arg
450 455 460

Ser Ala Glu Leu Leu Val Leu Ser Ala Lys Ser Ala Ala Ala Leu Asp
465 470 475 480

Ala Gln Ala Ala Arg Leu Ser Ala His Ile Ala Ala Tyr Pro Glu Gln
485 490 495

Gly Leu Gly Asp Val Ala Phe Ser Leu Val Ser Thr Arg Ser Pro Met
500 505 510

Glu His Arg Leu Ala Val Ala Ala Thr Ser Arg Glu Ala Leu Arg Ser
515 520 525

Ala Leu Glu Val Ala Ala Gln Gly Gln Thr Pro Ala Gly Ala Ala Arg
530 535 540

Gly Arg Ala Ala Ser Ser Pro Gly Lys Leu Ala Phe Leu Phe Ala Gly
545 550 555 560

Gln Gly Ala Gln Val Pro Gly Met Gly Arg Gly Leu Trp Glu Ala Trp
565 570 575

Pro Ala Phe Arg Glu Thr Phe Asp Arg Cys Val Thr Leu Phe Asp Arg
580 585 590

Glu Leu His Gln Pro Leu Cys Glu Val Met Trp Ala Glu Pro Gly Ser
595 600 605

Ser Arg Ser Ser Leu Leu Asp Gln Thr Ala Phe Thr Gln Pro Ala Leu
610 615 620

Phe Ala Leu Glu Tyr Ala Leu Ala Ala Leu Phe Arg Ser Trp Gly Val
625 630 635 640

Glu Pro Glu Leu Val Ala Gly His Ser Leu Gly Glu Leu Val Ala Ala
645 650 655

Cys Val Ala Gly Val Phe Ser Leu Glu Asp Ala Val Arg Leu Val Val
660 665 670

Ala Arg Gly Arg Leu Met Gln Ala Leu Pro Ala Gly Gly Ala Met Val
675 680 685

Ser Ile Ala Ala Pro Glu Ala Asp Val Ala Ala Ala Val Ala Pro His
690 695 700

Ala Ala Leu Val Ser Ile Ala Ala Val Asn Gly Pro Glu Gln Val Val
705 710 715 720

Ile Ala Gly Ala Glu Lys Phe Val Gln Gln Ile Ala Ala Ala Phe Ala
725 730 735

Ala Arg Gly Ala Arg Thr Lys Pro Leu His Val Ser His Ala Phe His
740 745 750

Ser Pro Leu Met Asp Pro Met Leu Glu Ala Phe Arg Arg Val Thr Glu
755 760 765

Ser Val Thr Tyr Arg Arg Pro Ser Ile Ala Leu Val Ser Asn Leu Ser
770 775 780

Gly Lys Pro Cys Thr Asp Glu Val Ser Ala Pro Gly Tyr Trp Val Arg
785 790 795 800

His Ala Arg Glu Ala Val Arg Phe Ala Asp Gly Val Lys Ala Leu His
805 810 815

Ala Ala Gly Ala Gly Leu Phe Val Glu Val Gly Pro Lys Pro Thr Leu
820 825 830

Leu Gly Leu Val Pro Ala Cys Leu Pro Asp Ala Arg Pro Val Leu Leu
835 840 845

Pro Ala Ser Arg Ala Gly Arg Asp Glu Ala Ala Ser Ala Leu Glu Ala
850 855 860

Leu Gly Gly Phe Trp Val Val Gly Gly Ser Val Thr Trp Ser Gly Val
865 870 875 880

Phe Pro Ser Gly Gly Arg Arg Val Pro Leu Pro Thr Tyr Pro Trp Gln
885 890 895

Arg Glu Arg Tyr Trp Ile Glu Ala Pro Val Asp Arg Glu Ala Asp Gly
900 905 910

Thr Gly Arg Ala Arg Ala Gly Gly His Pro Leu Leu Gly Glu Val Phe
915 920 925

Ser Val Ser Thr His Ala Gly Leu Arg Leu Trp Glu Thr Thr Leu Asp
930 935 940

Arg Lys Arg Leu Pro Trp Leu Gly Glu His Arg Ala Gln Gly Glu Val
945 950 955 960

Val Phe Pro Gly Ala Gly Tyr Leu Glu Met Ala Leu Ser Ser Gly Ala
965 970 975

Glu Ile Leu Gly Asp Gly Pro Ile Gln Val Thr Asp Val Val Leu Ile
980 985 990

Glu Thr Leu Thr Phe Ala Gly Asp Thr Ala Val Pro Val Gln Val Val
995 1000 1005

Thr Thr Glu Glu Arg Pro Gly Arg Leu Arg Phe Gln Val Ala Ser Arg
1010 1015 1020

Glu Pro Gly Glu Arg Arg Ala Pro Phe Arg Ile His Ala Arg Gly Val
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Leu Arg Arg Ile Gly Arg Val Glu Thr Pro Ala Arg Ser Asn Leu Ala
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Ala Leu Arg Ala Arg Leu His Ala Ala Val Pro Ala Ala Ala Ile Tyr
1060 1065 1070

Gly Ala Leu Ala Glu Met Gly Leu Gln Tyr Gly Pro Ala Leu Arg Gly
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Leu Ala Glu Leu Trp Arg Gly Glu Gly Glu Ala Leu Gly Arg Val Arg
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Leu Pro Glu Ala Ala Gly Ser Ala Thr Ala Tyr Gln Leu His Pro Val
1105 1110 1115 1120

Leu Leu Asp Ala Cys Val Gln Met Ile Val Gly Ala Phe Ala Asp Arg
1125 1130 1135

Asp Glu Ala Thr Pro Trp Ala Pro Val Glu Val Gly Ser Val Arg Leu
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Phe Gln Arg Ser Pro Gly Glu Leu Trp Cys His Ala Arg Val Val Ser
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Asp Gly Gln Gln Ala Ser Ser Arg Trp Ser Ala Asp Phe Glu Leu Met
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Asp Gly Thr Gly Ala Val Val Ala Glu Ile Ser Arg Leu Val Val Glu
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Arg Leu Ala Ser Gly Val Arg Arg Arg Asp Ala Asp Asp Trp Phe Leu
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Glu Leu Asp Trp Glu Pro Ala Ala Leu Gly Gly Pro Lys Ile Thr Ala
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Gly Arg Trp Leu Leu Leu Gly Glu Gly Gly Gly Leu Gly Arg Ser Leu
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Cys Ser Ala Leu Lys Ala Ala Gly His Val Val Val His Ala Ala Gly
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Asp Asp Thr Ser Thr Ala Gly Met Arg Ala Leu Leu Ala Asn Ala Phe
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Asp Gly Gln Ala Pro Thr Ala Val Val His Leu Ser Ser Leu Asp Gly
1285 1290 1295

Gly Gly Gln Leu Gly Pro Gly Leu Gly Ala Gln Gly Ala Leu Asp Ala
1300 1305 1310

Pro Arg Ser Pro Asp Val Asp Ala Asp Ala Leu Glu Ser Ala Leu Met
1315 1320 1325

Arg Gly Cys Asp Ser Val Leu Ser Leu Val Gln Ala Leu Val Gly Met
1330 1335 1340

Asp Leu Arg Asn Ala Pro Arg Leu Trp Leu Leu Thr Arg Gly Ala Gln
1345 1350 1355 1360

Ala Ala Ala Ala Gly Asp Val Ser Val Val Gln Ala Pro Leu Leu Gly

1365 1370 1375

Leu Gly Arg Thr Ile Ala Leu Glu His Ala Glu Leu Arg Cys Ile Ser
1380 1385 1390

Val Asp Leu Asp Pro Ala Glu Pro Glu Gly Glu Ala Asp Ala Leu Leu
1395 1400 1405

Ala Glu Leu Leu Ala Asp Asp Ala Glu Glu Glu Val Ala Leu Arg Gly
1410 1415 1420

Gly Asp Arg Leu Val Ala Arg Leu Val His Arg Leu Pro Asp Ala Gln
1425 1430 1435 1440

Arg Arg Glu Lys Val Glu Pro Ala Gly Asp Arg Pro Phe Arg Leu Glu
1445 1450 1455

Ile Asp Glu Pro Gly Ala Leu Asp Gln Leu Val Leu Arg Ala Thr Gly
1460 1465 1470

Arg Arg Ala Pro Gly Pro Gly Glu Val Glu Ile Ser Val Glu Ala Ala
1475 1480 1485

Gly Leu Asp Ser Ile Asp Ile Gln Leu Ala Leu Gly Val Ala Pro Asn
1490 1495 1500

Asp Leu Pro Gly Glu Glu Ile Glu Pro Leu Val Leu Gly Ser Glu Cys
1505 1510 1515 1520

Ala Gly Arg Ile Val Ala Val Gly Glu Gly Val Asn Gly Leu Val Val
1525 1530 1535

Gly Gln Pro Val Ile Ala Leu Ala Ala Gly Val Phe Ala Thr His Val
1540 1545 1550

Thr Thr Ser Ala Thr Leu Val Leu Pro Arg Pro Leu Gly Leu Ser Ala
1555 1560 1565

Thr Glu Ala Ala Ala Met Pro Leu Ala Tyr Leu Thr Ala Trp Tyr Ala
1570 1575 1580

Leu Asp Lys Val Ala His Leu Gln Ala Gly Glu Arg Val Leu Ile His
1585 1590 1595 1600

Ala Glu Ala Gly Gly Val Gly Leu Cys Ala Val Arg Trp Ala Gln Arg
1605 1610 1615

Val Gly Ala Glu Val Tyr Ala Thr Ala Asp Thr Pro Glu Asn Arg Ala
1620 1625 1630

Tyr Leu Glu Ser Leu Gly Val Arg Tyr Val Ser Asp Ser Arg Ser Gly
1635 1640 1645

Arg Phe Val Thr Asp Val His Ala Trp Thr Asp Gly Glu Gly Val Asp
1650 1655 1660

Val Val Leu Asp Ser Leu Ser Gly Glu Arg Ile Asp Lys Ser Leu Met
1665 1670 1675 1680

Val Leu Arg Ala Cys Gly Arg Leu Val Lys Leu Gly Arg Arg Asp Asp
1685 1690 1695

Cys Ala Asp Thr Gln Pro Gly Leu Pro Pro Leu Leu Arg Asn Phe Ser
1700 1705 1710

Phe Ser Gln Val Asp Leu Arg Gly Met Met Leu Asp Gln Pro Ala Arg
1715 1720 1725

Ile Arg Ala Leu Leu Asp Glu Leu Phe Gly Leu Val Ala Ala Gly Ala
1730 1735 1740

Ile Ser Pro Leu Gly Ser Gly Leu Arg Val Gly Gly Ser Leu Thr Pro
1745 1750 1755 1760

Pro Pro Val Glu Thr Phe Pro Ile Ser Arg Ala Ala Glu Ala Phe Arg
1765 1770 1775

Arg Met Ala Gln Gly Gln His Leu Gly Lys Leu Val Leu Thr Leu Asp
1780 1785 1790

Asp Pro Glu Val Arg Ile Arg Ala Pro Ala Glu Ser Ser Val Ala Val
1795 1800 1805

Arg Ala Asp Gly Thr Tyr Leu Val Thr Gly Gly Leu Gly Gly Leu Gly
1810 1815 1820

Leu Arg Val Ala Gly Trp Leu Ala Glu Arg Gly Ala Gly Gln Leu Val
1825 1830 1835 1840

Leu Val Gly Arg Ser Gly Ala Ala Ser Ala Glu Gln Arg Ala Ala Val
1845 1850 1855

Ala Ala Leu Glu Ala His Gly Ala Arg Val Thr Val Ala Lys Ala Asp
1860 1865 1870

Val Ala Asp Arg Ser Gln Ile Glu Arg Val Leu Arg Glu Val Thr Ala
1875 1880 1885

Ser Gly Met Pro Leu Arg Gly Val Val His Ala Ala Gly Leu Val Asp
1890 1895 1900

Asp Gly Leu Leu Met Gln Gln Thr Pro Ala Arg Phe Arg Thr Val Met
1905 1910 1915 1920

Gly Pro Lys Val Gln Gly Ala Leu His Leu His Thr Leu Thr Arg Glu
1925 1930 1935

Ala Pro Leu Ser Phe Phe Val Leu Tyr Ala Ser Ala Ala Gly Leu Phe
1940 1945 1950

Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
1955 1960 1965

Ala Leu Ser His His Arg Arg Ala Gln Gly Leu Pro Ala Leu Ser Ile
1970 1975 1980

Asp Trp Gly Met Phe Thr Glu Val Gly Met Ala Val Ala Gln Glu Asn
1985 1990 1995 2000

Arg Gly Ala Arg Gln Ile Ser Arg Gly Met Arg Gly Ile Thr Pro Asp
2005 2010 2015

Glu Gly Leu Ser Ala Leu Ala Arg Leu Leu Glu Gly Asp Arg Val Gln
2020 2025 2030

Thr Gly Val Ile Pro Ile Thr Pro Arg Gln Trp Val Glu Phe Tyr Pro
2035 2040 2045

Ala Thr Ala Ala Ser Arg Arg Leu Ser Arg Leu Val Thr Thr Gln Arg
2050 2055 2060

Ala Val Ala Asp Arg Thr Ala Gly Asp Arg Asp Leu Leu Glu Gln Leu
2065 2070 2075 2080

Ala Ser Ala Glu Pro Ser Ala Arg Ala Gly Leu Leu Gln Asp Val Val
2085 2090 2095

Arg Val Gln Val Ser His Val Leu Arg Leu Pro Glu Asp Lys Ile Glu
2100 2105 2110

Val Asp Ala Pro Leu Ser Ser Met Gly Met Asp Ser Leu Met Ser Leu
2115 2120 2125

Glu Leu Arg Asn Arg Ile Glu Ala Ala Leu Gly Val Ala Ala Pro Ala
2130 2135 2140

Ala Leu Gly Trp Thr Tyr Pro Thr Val Ala Ala Ile Thr Arg Trp Leu
2145 2150 2155 2160

Leu Asp Asp Ala Leu Val Val Arg Leu Gly Gly Gly Ser Asp Thr Asp
2165 2170 2175

Glu Ser Thr Ala Ser Ala Gly Ser Phe Val His Val Leu Arg Phe Arg
2180 2185 2190

Pro Val Val Lys Pro Arg Ala Arg Leu Phe Cys Phe His Gly Ser Gly
2195 2200 2205

Gly Ser Pro Glu Gly Phe Arg Ser Trp Ser Glu Lys Ser Glu Trp Ser
2210 2215 2220

Asp Leu Glu Ile Val Ala Met Trp His Asp Arg Ser Leu Ala Ser Glu
2225 2230 2235 2240

Asp Ala Pro Gly Lys Lys Tyr Val Gln Glu Ala Ala Ser Leu Ile Gln
2245 2250 2255

His Tyr Ala Asp Ala Pro Phe Ala Leu Val Gly Phe Ser Leu Gly Val
2260 2265 2270

Arg Phe Val Met Gly Thr Ala Val Glu Leu Ala Ser Arg Ser Gly Ala
2275 2280 2285

Pro Ala Pro Leu Ala Val Phe Thr Leu Gly Gly Ser Leu Ile Ser Ser
2290 2295 2300

Ser Glu Ile Thr Pro Glu Met Glu Thr Asp Ile Ile Ala Lys Leu Phe
2305 2310 2315 2320

Phe Arg Asn Ala Ala Gly Phe Val Arg Ser Thr Gln Gln Val Gln Ala
2325 2330 2335

Asp Ala Arg Ala Asp Lys Val Ile Thr Asp Thr Met Val Ala Pro Ala
2340 2345 2350

Pro Gly Asp Ser Lys Glu Pro Pro Val Lys Ile Ala Val Pro Ile Val
2355 2360 2365

Ala Ile Ala Gly Ser Asp Asp Val Ile Val Pro Pro Ser Asp Val Gln
2370 2375 2380

Asp Leu Gln Ser Arg Thr Thr Glu Arg Phe Tyr Met His Leu Leu Pro
2385 2390 2395 2400

Gly Asp His Glu Phe Leu Val Asp Arg Gly Arg Glu Ile Met His Ile

2405 2410 2415

Val Asp Ser His Leu Asn Pro Leu Leu Ala Ala Arg Thr Thr Ser Ser
2420 2425 2430

Gly Pro Ala Phe Glu Ala Lys
2435

<210> 8
<211> 419
<212> PRT
<213> Sorangium cellulosum

<400> 8
Met Thr Gln Glu Gln Ala Asn Gln Ser Glu Thr Lys Pro Ala Phe Asp
1 5 10 15

Phe Lys Pro Phe Ala Pro Gly Tyr Ala Glu Asp Pro Phe Pro Ala Ile
20 25 30

Glu Arg Leu Arg Glu Ala Thr Pro Ile Phe Tyr Trp Asp Glu Gly Arg
35 40 45

Ser Trp Val Leu Thr Arg Tyr His Asp Val Ser Ala Val Phe Arg Asp
50 55 60

Glu Arg Phe Ala Val Ser Arg Glu Glu Trp Glu Ser Ser Ala Glu Tyr
65 70 75 80

Ser Ser Ala Ile Pro Glu Leu Ser Asp Met Lys Lys Tyr Gly Leu Phe
85 90 95

Gly Leu Pro Pro Glu Asp His Ala Arg Val Arg Lys Leu Val Asn Pro
100 105 110

Ser Phe Thr Ser Arg Ala Ile Asp Leu Leu Arg Ala Glu Ile Gln Arg
115 120 125

Thr Val Asp Gln Leu Leu Asp Ala Arg Ser Gly Gln Glu Glu Phe Asp
130 135 140

Val Val Arg Asp Tyr Ala Glu Gly Ile Pro Met Arg Ala Ile Ser Ala
145 150 155 160

Leu Leu Lys Val Pro Ala Glu Cys Asp Glu Lys Phe Arg Arg Phe Gly
165 170 175

Ser Ala Thr Ala Arg Ala Leu Gly Val Gly Leu Val Pro Gln Val Asp
180 185 190

Glu Glu Thr Lys Thr Leu Val Ala Ser Val Thr Glu Gly Leu Ala Leu
195 200 205

Leu His Asp Val Leu Asp Glu Arg Arg Arg Asn Pro Leu Glu Asn Asp
210 215 220

Val Leu Thr Met Leu Leu Gln Ala Glu Ala Asp Gly Ser Arg Leu Ser
225 230 235 240

Thr Lys Glu Leu Val Ala Leu Val Gly Ala Ile Ile Ala Ala Gly Thr
245 250 255

Asp Thr Thr Ile Tyr Leu Ile Ala Phe Ala Val Leu Asn Leu Leu Arg
260 265 270

Ser Pro Glu Ala Leu Glu Leu Val Lys Ala Glu Pro Gly Leu Met Arg
275 280 285

Asn Ala Leu Asp Glu Val Leu Arg Phe Asp Asn Ile Leu Arg Ile Gly
290 295 300

Thr Val Arg Phe Ala Arg Gln Asp Leu Glu Tyr Cys Gly Ala Ser Ile
305 310 315 320

Lys Lys Gly Glu Met Val Phe Leu Leu Ile Pro Ser Ala Leu Arg Asp
325 330 335

Gly Thr Val Phe Ser Arg Pro Asp Val Phe Asp Val Arg Arg Asp Thr
340 345 350

Gly Ala Ser Leu Ala Tyr Gly Arg Gly Pro His Val Cys Pro Gly Val
355 360 365

Ser Leu Ala Arg Leu Glu Ala Glu Ile Ala Val Gly Thr Ile Phe Arg
370 375 380

Arg Phe Pro Glu Met Lys Leu Lys Glu Thr Pro Val Phe Gly Tyr His
385 390 395 400

Pro Ala Phe Arg Asn Ile Glu Ser Leu Asn Val Ile Leu Lys Pro Ser
405 410 415

Lys Ala Gly

<210> 9
<211> 607
<212> PRT
<213> Sorangium cellulosum

<400> 9
Ala Ser Leu Asp Ala Leu Phe Ala Arg Ala Thr Ser Ala Arg Val Leu
1 5 10 15

Asp Asp Gly His Gly Arg Ala Thr Glu Arg His Val Leu Ala Glu Ala
20 25 30

Arg Gly Ile Glu Asp Leu Arg Ala Leu Arg Glu His Leu Arg Ile Gln
35 40 45

Glu Gly Gly Pro Ser Phe His Cys Met Cys Leu Gly Asp Leu Thr Val
50 55 60

Glu Leu Leu Ala His Asp Gln Pro Leu Ala Ser Ile Ser Phe His His
65 70 75 80

Ala Arg Ser Leu Arg His Pro Asp Trp Thr Ser Asp Ala Met Leu Val
85 90 95

Asp Gly Pro Ala Leu Val Arg Trp Leu Ala Ala Arg Gly Ala Pro Gly
100 105 110

Pro Leu Arg Glu Tyr Glu Glu Glu Arg Glu Arg Ala Arg Thr Ala Gln
115 120 125

Glu Ala Arg Arg Leu Trp Leu Ala Ala Ala Pro Pro Cys Phe Ala Pro
130 135 140

Asp Leu Pro Arg Phe Glu Asp Asp Ala Asn Gly Leu Pro Leu Gly Pro
145 150 155 160

Met Ser Pro Glu Val Ala Glu Ala Glu Arg Arg Leu Arg Ala Ser Tyr
165 170 175

Ala Thr Pro Glu Leu Ala Cys Ala Ala Leu Leu Ala Trp Leu Gly Thr
180 185 190

Gly Ala Gly Pro Trp Ser Gly Tyr Pro Ala Tyr Glu Met Leu Pro Glu
195 200 205

Asn Leu Leu Leu Gly Phe Gly Leu Pro Thr Ala Ile Ala Ala Ala Ser
210 215 220

Ala Pro Gly Thr Ser Glu Ala Ala Leu Arg Gly Ala Ala Arg Leu Phe
225 230 235 240

Ala Ser Trp Glu Val Val Ser Ser Lys Lys Ser Gln Leu Gly Asn Ile
245 250 255

Pro Glu Ala Leu Trp Glu Arg Leu Arg Thr Ile Val Arg Ala Met Gly
260 265 270

Asn Ala Asp Asn Leu Ser Arg Phe Glu Arg Ala Glu Ala Ile Ala Ala
275 280 285

Glu Val Arg Arg Leu Arg Ala Gln Pro Ala Pro Phe Ala Ala Gly Ala
290 295 300

Gly Leu Ala Val Ala Gly Val Ser Ser Ser Gly Arg Leu Ser Gly Leu
305 310 315 320

Val Thr Asp Gly Asp Ala Leu Tyr Ser Gly Asp Gly Asn Asp Ile Val
325 330 335

Met Phe Gln Pro Gly Arg Ile Ser Pro Val Val Leu Leu Ala Gly Thr
340 345 350

Asp Pro Phe Phe Glu Leu Ala Pro Pro Leu Ser Gln Met Leu Phe Val
355 360 365

Ala His Ala Asn Ala Gly Thr Ile Ser Lys Val Leu Thr Glu Gly Ser
370 375 380

Pro Leu Ile Val Met Ala Arg Asn Gln Ala Arg Pro Met Ser Leu Val
385 390 395 400

His Ala Arg Gly Phe Met Ala Trp Val Asn Gln Ala Met Val Pro Asp
405 410 415

Pro Glu Arg Gly Ala Pro Phe Val Val Gln Arg Ser Thr Ile Met Glu
420 425 430

Phe Glu His Pro Thr Pro Arg Cys Leu His Glu Pro Ala Gly Ser Ala
435 440 445

Phe Ser Leu Ala Cys Asp Glu Glu His Leu Tyr Trp Cys Glu Leu Ser
450 455 460

Ala Gly Arg Leu Glu Leu Trp Arg His Pro His His Arg Pro Gly Ala
465 470 475 480

Pro Ser Arg Phe Ala Tyr Leu Gly Glu His Pro Ile Ala Ala Thr Trp
485 490 495

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Tyr Pro Ser Leu Thr Leu Asn Ala Thr His Val Leu Trp Ala Asp Pro
            500                 505                 510

Asp Arg Arg Ala Ile Leu Gly Val Asp Lys Arg Thr Gly Val Glu Pro
        515                 520                 525

Ile Val Leu Ala Glu Thr Arg His Pro Pro Ala His Val Val Ser Glu
    530                 535                 540

Asp Arg Asp Ile Phe Ala Leu Thr Gly Gln Pro Asp Ser Arg Asp Trp
545                 550                 555                 560

His Val Glu His Ile Arg Ser Gly Ala Ser Thr Val Val Ala Asp Tyr
                565                 570                 575

Gln Arg Gln Leu Trp Asp Arg Pro Asp Met Val Leu Asn Arg Arg Gly
            580                 585                 590

Leu Phe Phe Thr Thr Asn Asp Arg Ile Leu Thr Leu Ala Arg Ser
        595                 600                 605


<210> 10
<211> 423
<212> PRT
<213> Sorangium cellulosum

<400> 10
Met Gly Ala Leu Ile Ser Val Ala Ala Pro Gly Cys Ala Leu Gly Gly
  1               5                  10                  15

Ala Glu Glu Glu Gly Gln Pro Gly Gln Asp Ala Gly Ala Gly Ala Leu
            20                  25                  30

Ala Pro Ala Arg Glu Val Met Ala Ala Glu Val Ala Ala Gly Gln Met
        35                  40                  45

Pro Gly Ala Val Trp Leu Val Ala Arg Gly Asp Asp Val His Val Asp
    50                  55                  60

Ala Val Gly Val Thr Glu Leu Gly Gly Ser Ala Pro Met Arg Arg Asp
65                  70                  75                  80

Thr Ile Phe Arg Ile Ala Ser Met Thr Lys Ala Val Thr Ala Thr Ala
                85                  90                  95

Val Met Met Leu Val Glu Glu Gly Lys Leu Asp Leu Asp Ser Pro Val
            100                 105                 110

Asp Arg Trp Leu Pro Glu Leu Ala Asn Arg Lys Val Leu Ala Arg Ile
        115                 120                 125

Asp Gly Pro Ile Asp Glu Thr Val Pro Ala Glu Arg Pro Ile Thr Val
    130                 135                 140

Arg Asp Leu Met Thr Phe Thr Met Gly Phe Gly Ile Ser Phe Asp Ala
145                 150                 155                 160

Ser Ser Pro Ile Gln Arg Ala Ile Asp Glu Leu Gly Leu Val Asn Ala
                165                 170                 175

Gln Pro Val Pro Met Thr Pro His Gly Pro Asp Glu Trp Ile Arg Arg
            180                 185                 190
```

Leu Gly Thr Leu Pro Leu Met His Gln Pro Gly Ala Gln Trp Met Tyr
195 200 205

Asn Thr Gly Ser Leu Val Gln Gly Val Leu Val Gly Arg Ala Ala Asp
210 215 220

Gln Gly Phe Asp Ala Phe Val Arg Glu Arg Ile Leu Ala Pro Leu Gly
225 230 235 240

Met Arg Asp Thr Asp Phe His Val Pro Ala Asp Lys Leu Ala Arg Phe
245 250 255

Ala Gly Cys Gly Tyr Phe Thr Asp Glu Gln Thr Gly Glu Lys Thr Arg
260 265 270

Met Asp Arg Asp Gly Ala Glu Ser Ala Tyr Ala Ser Pro Pro Ala Phe
275 280 285

Pro Ser Gly Ala Ala Gly Leu Val Ser Thr Val Asp Asp Tyr Leu Leu
290 295 300

Phe Ala Arg Met Leu Met Asn Gly Gly Val His Glu Gly Arg Arg Leu
305 310 315 320

Leu Ser Ala Ala Ser Val Arg Glu Met Thr Ala Asp His Leu Thr Pro
325 330 335

Ala Gln Lys Ala Ala Ser Ser Phe Phe Pro Gly Phe Phe Glu Thr His
340 345 350

Gly Trp Gly Tyr Gly Met Ala Val Val Thr Ala Pro Asp Ala Val Ser
355 360 365

Glu Val Pro Gly Arg Tyr Gly Trp Asp Gly Gly Phe Gly Thr Ser Trp
370 375 380

Ile Asn Asp Pro Gly Arg Glu Leu Ile Gly Ile Val Met Thr Gln Ser
385 390 395 400

Ala Gly Phe Leu Phe Ser Gly Ala Leu Glu Arg Phe Trp Arg Ser Val
405 410 415

Tyr Val Ala Thr Glu Ser Ala
420

<210> 11
<211> 713
<212> PRT
<213> Sorangium cellulosum

<400> 11
Met His Gly Leu Thr Glu Arg Gln Val Leu Leu Ser Leu Val Thr Leu
1 5 10 15

Ala Leu Ile Leu Val Thr Ala Arg Ala Ser Gly Glu Leu Ala Arg Arg
20 25 30

Leu Arg Gln Pro Glu Val Leu Gly Glu Leu Phe Gly Gly Val Val Leu
35 40 45

Gly Pro Ser Val Val Gly Ala Leu Ala Pro Gly Phe His Arg Ala Leu
50 55 60

Phe Gln Glu Pro Ala Val Gly Val Val Leu Ser Gly Ile Ser Trp Ile

65 70 75 80

Gly Ala Leu Leu Leu Leu Leu Met Ala Gly Ile Glu Val Asp Val Gly
85 90 95

Ile Leu Arg Lys Glu Ala Arg Pro Gly Ala Leu Ser Ala Leu Gly Ala
100 105 110

Ile Ala Pro Pro Leu Ala Ala Gly Ala Ala Phe Ser Ala Leu Val Leu
115 120 125

Asp Arg Pro Leu Pro Ser Gly Leu Phe Leu Gly Ile Val Leu Ser Val
130 135 140

Thr Ala Val Ser Val Ile Ala Lys Val Leu Ile Glu Arg Glu Ser Met
145 150 155 160

Arg Arg Ser Tyr Ala Gln Val Thr Leu Ala Ala Gly Val Val Ser Glu
165 170 175

Val Ala Ala Trp Val Leu Val Ala Met Thr Ser Ser Ser Tyr Gly Ala
180 185 190

Ser Pro Ala Leu Ala Val Ala Arg Ser Ala Leu Leu Ala Ser Gly Phe
195 200 205

Leu Leu Phe Met Val Leu Val Gly Arg Arg Leu Thr His Leu Ala Met
210 215 220

Arg Trp Val Ala Asp Ala Thr Arg Val Ser Lys Gly Gln Val Ser Leu
225 230 235 240

Val Leu Val Leu Thr Phe Leu Ala Ala Ala Leu Thr Gln Arg Leu Gly
245 250 255

Leu His Pro Leu Leu Gly Ala Phe Ala Leu Gly Val Leu Leu Asn Ser
260 265 270

Ala Pro Arg Thr Asn Arg Pro Leu Leu Asp Gly Val Gln Thr Leu Val
275 280 285

Ala Gly Leu Phe Ala Pro Val Phe Phe Val Leu Ala Gly Met Arg Val
290 295 300

Asp Val Ser Gln Leu Arg Thr Pro Ala Ala Trp Gly Thr Val Ala Leu
305 310 315 320

Leu Leu Ala Thr Ala Thr Ala Ala Lys Val Val Pro Ala Ala Leu Gly
325 330 335

Ala Arg Leu Gly Gly Leu Arg Gly Ser Glu Ala Ala Leu Val Ala Val
340 345 350

Gly Leu Asn Met Lys Gly Gly Thr Asp Leu Ile Val Ala Ile Val Gly
355 360 365

Val Glu Leu Gly Leu Leu Ser Asn Glu Ala Tyr Thr Met Tyr Ala Val
370 375 380

Val Ala Leu Val Thr Val Thr Ala Ser Pro Ala Leu Leu Ile Trp Leu
385 390 395 400

Glu Lys Arg Ala Pro Pro Thr Gln Glu Glu Ser Ala Arg Leu Glu Arg
405 410 415

Glu Glu Ala Ala Arg Arg Ala Tyr Ile Pro Gly Val Glu Arg Ile Leu
420 425 430

Val Pro Ile Val Ala His Ala Leu Pro Gly Phe Ala Thr Asp Ile Val
435 440 445

Glu Ser Ile Val Ala Ser Lys Arg Lys Leu Gly Glu Thr Val Asp Ile
450 455 460

Thr Glu Leu Ser Val Glu Gln Gln Ala Pro Gly Pro Ser Arg Ala Ala
465 470 475 480

Gly Glu Ala Ser Arg Gly Leu Ala Arg Leu Gly Ala Arg Leu Arg Val
485 490 495

Gly Ile Trp Arg Gln Arg Arg Glu Leu Arg Gly Ser Ile Gln Ala Ile
500 505 510

Leu Arg Ala Ser Arg Asp His Asp Leu Leu Val Ile Gly Ala Arg Ser
515 520 525

Pro Ala Arg Ala Arg Gly Met Ser Phe Gly Arg Leu Gln Asp Ala Ile
530 535 540

Val Gln Arg Ala Glu Ser Asn Val Leu Val Val Val Gly Asp Pro Pro
545 550 555 560

Ala Ala Glu Arg Ala Ser Ala Arg Arg Ile Leu Val Pro Ile Ile Gly
565 570 575

Leu Glu Tyr Ser Phe Ala Ala Ala Asp Leu Ala Ala His Val Ala Leu
580 585 590

Ala Trp Asp Ala Glu Leu Val Leu Leu Ser Ser Ala Gln Thr Asp Pro
595 600 605

Gly Ala Val Val Trp Arg Asp Arg Glu Pro Ser Arg Val Arg Ala Val
610 615 620

Ala Arg Ser Val Val Asp Glu Ala Val Phe Arg Gly Arg Arg Leu Gly
625 630 635 640

Val Arg Val Ser Ser Arg Val His Val Gly Ala His Pro Ser Asp Glu
645 650 655

Ile Thr Arg Glu Leu Ala Arg Ala Pro Tyr Asp Leu Leu Val Leu Gly
660 665 670

Cys Tyr Asp His Gly Pro Leu Gly Arg Leu Tyr Leu Gly Ser Thr Val
675 680 685

Glu Ser Val Val Val Arg Ser Arg Val Pro Val Ala Leu Leu Val Ala
690 695 700

His Gly Gly Thr Arg Glu Gln Val Arg
705 710

<210> 12
<211> 126
<212> PRT
<213> Sorangium cellulosum

<400> 12
Met Asp Lys Pro Ile Gly Arg Thr Arg Cys Ala Ile Ala Glu Gly Tyr

```
1               5                  10                  15
Ile Pro Gly Gly Ser Asn Gly Pro Glu Pro Gln Met Thr Ser His Glu
            20                  25                  30
Thr Ala Cys Leu Leu Asn Ala Ser Asp Arg Asp Ala Gln Val Ala Ile
        35                  40                  45
Thr Val Tyr Phe Ser Asp Arg Asp Pro Ala Gly Pro Tyr Arg Val Thr
    50                  55                  60
Val Pro Ala Arg Arg Thr Arg His Val Arg Phe Asn Asp Leu Thr Glu
65                  70                  75                  80
Pro Glu Pro Ile Pro Arg Asp Thr Asp Tyr Ala Ser Val Ile Glu Ser
                85                  90                  95
Asp Ala Pro Ile Val Val Gln His Thr Arg Leu Asp Ser Arg Gln Ala
            100                 105                 110
Glu Asn Ala Leu Leu Ser Thr Ile Ala Tyr Thr Asp Arg Glu
        115                 120                 125
```

<210> 13
<211> 149
<212> PRT
<213> Sorangium cellulosum

```
<400> 13
Met Lys His Val Asp Thr Gly Arg Arg Phe Gly Arg Arg Ile Gly His
  1               5                  10                  15
Thr Leu Gly Leu Leu Ala Ser Met Ala Leu Ala Gly Cys Gly Gly Pro
            20                  25                  30
Ser Glu Lys Thr Val Gln Gly Thr Arg Leu Ala Pro Gly Ala Asp Ala
        35                  40                  45
Arg Val Thr Ala Asp Val Asp Pro Asp Ala Ala Thr Thr Arg Leu Ala
    50                  55                  60
Val Asp Val Val His Leu Ser Pro Pro Glu Arg Leu Glu Ala Gly Ser
65                  70                  75                  80
Glu Arg Phe Val Val Trp Gln Arg Pro Ser Pro Glu Ser Pro Trp Arg
                85                  90                  95
Arg Val Gly Val Leu Asp Tyr Asn Ala Asp Ser Arg Arg Gly Lys Leu
            100                 105                 110
Ala Glu Thr Thr Val Pro Tyr Ala Asn Phe Glu Leu Leu Ile Thr Ala
        115                 120                 125
Glu Lys Gln Ser Ser Pro Gln Ser Pro Ser Ser Ala Ala Val Ile Gly
    130                 135                 140
Pro Thr Ser Val Gly
145
```

<210> 14
<211> 184
<212> PRT
<213> Sorangium cellulosum

<400> 14
Val Thr Ser Glu Glu Val Pro Gly Ala Ala Leu Gly Ala Gln Ser Ser
1 5 10 15

Leu Val Arg Ala Gln His Ala Ala Arg His Val Arg Pro Cys Thr Arg
20 25 30

Ala Glu Glu Pro Pro Ala Leu Met His Gly Leu Thr Glu Arg Gln Val
35 40 45

Leu Leu Ser Leu Val Ala Leu Ala Leu Val Leu Leu Thr Ala Arg Ala
50 55 60

Phe Gly Glu Leu Ala Arg Arg Leu Arg Gln Pro Glu Val Leu Gly Glu
65 70 75 80

Leu Phe Gly Gly Val Val Leu Gly Pro Ser Val Val Gly Ala Leu Ala
85 90 95

Pro Gly Phe His Arg Val Leu Phe Gln Asp Pro Ala Val Gly Val Val
100 105 110

Leu Ser Gly Ile Ser Trp Ile Gly Ala Leu Val Leu Leu Leu Met Ala
115 120 125

Gly Ile Glu Val Asp Val Ser Ile Leu Arg Lys Glu Ala Arg Pro Gly
130 135 140

Ala Leu Ser Ala Leu Gly Ala Ile Ala Pro Pro Leu Arg Thr Pro Gly
145 150 155 160

Pro Leu Val Gln Arg Met Gln Gly Ala Phe Thr Trp Asp Leu Asp Val
165 170 175

Ser Pro Arg Arg Ser Ala Gln Ala
180

<210> 15
<211> 145
<212> PRT
<213> Sorangium cellulosum

<400> 15
Val Asn Ala Pro Cys Met Arg Cys Thr Ser Gly Pro Gly Val Arg Ser
1 5 10 15

Gly Gly Ala Ile Ala Pro Ser Ala Glu Ser Ala Pro Gly Arg Ala Ser
20 25 30

Leu Arg Arg Met Leu Thr Ser Thr Ser Ile Pro Ala Met Ser Ser Arg
35 40 45

Thr Ser Ala Pro Ile Gln Glu Met Pro Glu Ser Thr Thr Pro Thr Ala
50 55 60

Gly Ser Trp Lys Arg Thr Arg Trp Asn Pro Gly Ala Ser Ala Pro Thr
65 70 75 80

Thr Asp Gly Pro Ser Thr Thr Pro Pro Lys Ser Ser Pro Ser Thr Ser
85 90 95

Gly Trp Arg Ser Arg Arg Ala Ser Ser Pro Lys Ala Arg Ala Val Arg
100 105 110

Arg Thr Ser Ala Arg Ala Thr Ser Glu Ser Arg Thr Cys Arg Ser Val
115 120 125

Arg Pro Cys Ile Arg Ala Gly Gly Ser Ser Ala Arg Val Gln Gly Arg
130 135 140

Thr
145

<210> 16
<211> 185
<212> PRT
<213> Sorangium cellulosum

<400> 16
Val Leu Ala Pro Pro Ala Asp Ile Arg Pro Pro Ala Ala Ala Gln Leu
1 5 10 15

Glu Pro Asp Ser Pro Asp Asp Glu Ala Asp Glu Ala Asp Glu Ala Leu
20 25 30

Arg Pro Phe Arg Asp Ala Ile Ala Ala Tyr Ser Glu Ala Val Arg Trp
35 40 45

Ala Glu Ala Ala Gln Arg Pro Arg Leu Glu Ser Leu Val Arg Leu Ala
50 55 60

Ile Val Arg Leu Gly Lys Ala Leu Asp Lys Val Pro Phe Ala His Thr
65 70 75 80

Thr Ala Gly Val Ser Gln Ile Ala Gly Arg Leu Gln Asn Asp Ala Val
85 90 95

Trp Phe Asp Val Ala Ala Arg Tyr Ala Ser Phe Arg Ala Ala Thr Glu
100 105 110

His Ala Leu Arg Asp Ala Ala Ser Ala Met Glu Ala Leu Ala Ala Gly
115 120 125

Pro Tyr Arg Gly Ser Ser Arg Val Ser Ala Ala Val Gly Glu Phe Arg
130 135 140

Gly Glu Ala Ala Arg Leu His Pro Ala Asp Arg Val Pro Ala Ser Asp
145 150 155 160

Gln Gln Ile Leu Thr Ala Leu Arg Ala Ala Glu Arg Ala Leu Ile Ala
165 170 175

Leu Tyr Thr Ala Phe Ala Arg Glu Glu
180 185

<210> 17
<211> 146
<212> PRT
<213> Sorangium cellulosum

<400> 17
Met Ala Asp Ala Ala Ser Arg Ser Ala Cys Ser Val Ala Ala Arg Lys
1 5 10 15

Leu Ala Tyr Arg Ala Ala Thr Ser Asn Gln Thr Ala Ser Phe Trp Ser
20 25 30

Leu Pro Ala Ile Trp Glu Thr Pro Ala Val Val Cys Ala Lys Gly Thr
35 40 45

Leu Ser Ser Ala Leu Pro Ser Arg Thr Ile Ala Ser Arg Thr Arg Leu
50 55 60

Ser Ser Arg Gly Arg Cys Ala Ala Ser Ala His Arg Thr Ala Ser Glu
65 70 75 80

Tyr Ala Ala Ile Ala Ser Arg Asn Gly Arg Ser Ala Ser Ser Ala Ser
85 90 95

Ser Ala Ser Ser Ser Gly Glu Ser Gly Ser Ser Trp Ala Ala Ala Gly
100 105 110

Gly Arg Met Ser Ala Gly Gly Ala Ser Thr Gly Glu Val Tyr Glu Gln
115 120 125

Ala Pro Arg Leu Arg Leu Ala Gln Ser Val Ala Ala Arg Arg Arg Asp
130 135 140

Pro Thr
145

<210> 18
<211> 288
<212> PRT
<213> Sorangium cellulosum

<400> 18
Val Thr Val Ser Ser Met Pro Arg Ser Trp Ser Ser Arg Val Arg Thr
1 5 10 15

Val Val Thr Ala Leu Gly Cys Ala Arg Arg Leu Ser Gly Ser Ile Ser
20 25 30

Arg Leu Arg Arg His Pro Glu Ala Gly Arg Ala Pro Arg Ser Arg Leu
35 40 45

Arg Ala Trp Arg Arg Leu Pro Gln His Ile Ser Ser Pro Trp Arg His
50 55 60

Leu Pro Pro Gly Ala Arg Val Gly Thr Ser Cys Pro Ala Asp Arg Arg
65 70 75 80

Ile Leu Pro Ser His Arg Thr Ala Asp Leu Gly Thr Ser Gly Gly Thr
85 90 95

Leu Val Ala Arg Met Ser Gly His Val Ala Arg Asn Pro His Ala Ala
100 105 110

Val Leu Val Gly Asp Gly Ser Ala Arg Gly Arg Arg Arg Leu Ser Asn
115 120 125

Arg Arg Ala Glu Arg Arg Val Ser Asp Val Thr Cys Arg Glu Gly Gly
130 135 140

Glu Ala Met Gln Lys Ile Ala Gly Lys Leu Val Val Gly Leu Ile Ser
145 150 155 160

Val Ser Gly Met Ser Leu Leu Ala Ala Cys Gly Gly Glu Lys Arg Ser
165 170 175

```
Gly Gly Glu Ala Gln Thr Pro Gly Gly Ala Gln Gly Glu Ala Pro Val
            180                 185                 190

Pro Val Gly Ser Ala Val Asp Ser Ile Val Ala Ala Arg Cys Asp Arg
        195                 200                 205

Glu Ala Arg Cys Asn Asn Ile Gly Gln Asp Arg Glu Tyr Ser Ser Lys
    210                 215                 220

Asp Ala Cys Ser Asn Lys Ile Arg Ser Glu Trp Arg Asp Glu Leu Thr
225                 230                 235                 240

Phe Gly Glu Cys Pro Gly Gly Ile Asp Ala Lys Gln Leu Asn Glu Cys
                245                 250                 255

Leu Glu Gly Ile Arg Asn Glu Gly Cys Gly Asn Pro Phe Asp Thr Leu
            260                 265                 270

Gly Arg Val Val Ala Cys Arg Ser Ser Asp Leu Cys Arg Asp Ala Arg
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<213> Sorangium cellulosum

<400> 19

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Val Val Thr Ala Leu Gly Cys Ala Arg Arg Leu Ser Gly Ser Ile Ser
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Arg Leu Arg Arg His Pro Glu Ala Gly Arg Ala Pro Arg Ser Arg Leu
        35                  40                  45

Arg Ala Trp Arg Arg Leu Pro Gln His Ile Ser Ser Pro Trp Arg His
    50                  55                  60

Leu Pro Pro Gly Ala Arg Val Gly Thr Ser Cys Pro Ala Asp Arg Arg
65                  70                  75                  80

Ile Leu Pro Ser His Arg Thr Ala Asp Leu Gly Thr Ser Gly Gly Thr
                85                  90                  95

Leu Val Ala Arg Met Ser Gly His Val Ala Arg Asn Pro His Ala Ala
            100                 105                 110

Val Leu Val Gly Asp Gly Ser Ala Arg Gly Arg Arg Arg Leu Ser Asn
        115                 120                 125

Arg Arg Ala Glu Arg Arg Val Ser Asp Val Thr Cys Arg Glu Gly Gly
    130                 135                 140

Glu Ala Met Gln Lys Ile Ala Gly Lys Leu Val Val Gly Leu Ile Ser
145                 150                 155                 160

Val Ser Gly Met Ser Leu Leu Ala Ala Cys Gly Gly Glu Lys Arg Ser
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Gly Gly Glu Ala Gln Thr Pro Gly Gly Ala Gln Gly Glu Ala Pro Val
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            180                 185                 190

Pro Val Gly Ser Ala Val Asp Ser Ile Val Ala Ala Arg Cys Asp Arg
        195                 200                 205

Glu Ala Arg Cys Asn Asn Ile Gly Gln Asp Arg Glu Tyr Ser Ser Lys
    210                 215                 220

Asp Ala Cys Ser Asn Lys Ile Arg Ser Glu Trp Arg Asp Glu Leu Thr
225                 230                 235                 240

Phe Gly Glu Cys Pro Gly Gly Ile Asp Ala Lys Gln Leu Asn Glu Cys
                245                 250                 255

Leu Glu Gly Ile Arg Asn Glu Gly Cys Gly Asn Pro Phe Asp Thr Leu
            260                 265                 270

Gly Arg Val Val Ala Cys Arg Ser Ser Asp Leu Cys Arg Asp Ala Arg
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Pro Ile Gly Arg Thr Arg Trp Ala Ile Ala Glu Gly Tyr Ile Pro Gly
         35                  40                  45

Arg Ser Asn Gly Pro Glu Pro Gln Met Thr Ser His Glu Thr Ala Cys
     50                  55                  60

Leu Leu Asn Ala Ser Asp Arg Asp Ala Gln Val Ala Ile Thr Val Tyr
 65                  70                  75                  80

Phe Ser Asp Arg Asp Pro Ala Gly Pro Tyr Arg Val Thr Val Pro Ala
                 85                  90                  95

Arg Arg Thr Arg His Val Arg Phe Asn Asp Leu Thr Glu Pro Glu Pro
            100                 105                 110

Ile Pro Arg Asp Thr Asp Tyr Ala Ser Val Ile Glu Ser Asp Val Pro
        115                 120                 125

Ile Val Val Gln His Thr Arg Leu Asp Ser Arg Gln Ala Glu Asn Ala
    130                 135                 140

Leu Ile Ser Thr Ile Ala Tyr Thr Asp Arg Glu
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35 40 45

Leu Ala Pro Gly Ala Asp Ala His Val Ala Ala Asp Val Asp Pro Asp
50 55 60

Ala Ala Thr Thr Arg Leu Ala Val Asp Val Val His Leu Ser Pro Pro
65 70 75 80

Glu Arg Ile Glu Ala Gly Ser Glu Arg Phe Val Val Trp Gln Arg Pro
85 90 95

Ser Ser Glu Ser Pro Trp Gln Arg Val Gly Val Leu Asp Tyr Asn Ala
100 105 110

Ala Ser Arg Arg Gly Lys Leu Ala Glu Thr Thr Val Pro His Ala Asn
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Ser Ser Ala Ala Val Ile Gly Pro Thr Ser Val Gly
145 150 155

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35 40 45

Gly Leu Leu Leu Leu Leu Gly Lys His Arg Ser Ala Arg Pro Pro Asp
50 55 60

Ala Glu His Pro Phe Gly His Gly Lys Glu Leu Tyr Phe Trp Thr Leu
65 70 75 80

Ile Val Ala Ile Met Ile Phe Ala Ala Gly Gly Gly Val Ser Ile Tyr
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Glu Gly Ile Leu His Leu Leu His Pro Arg Gln Ile Glu Asp Pro Thr
100 105 110

Trp Asn Tyr Val Val Leu Gly Ala Ala Ala Val Phe Glu Gly Thr Ser
115 120 125

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145 150 155 160

Leu Glu Asp Ser Ala Ala Leu Ala Gly Leu Thr Ile Ala Phe Leu Gly
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Val Trp Leu Gly His Arg Leu Gly Asn Pro Tyr Leu Asp Gly Ala Ala
180 185 190

Ser Ile Gly Ile Gly Leu Val Leu Ala Ala Val Ala Val Phe Leu Ala
195 200 205

Ser Gln Ser Arg Gly Leu Leu Val Gly Glu Ser Ala Asp Arg Glu Leu
210 215 220

Leu Ala Ala Ile Arg Ala Leu Ala Ser Ala Asp Pro Gly Val Ser Ala
225 230 235 240

Val Gly Arg Pro Leu Thr Met His Phe Gly Pro His Glu Val Leu Val
245 250 255

Val Leu Arg Ile Glu Phe Asp Ala Ala Leu Thr Ala Ser Gly Val Ala
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Val Lys His Ile Tyr Val Glu Ala Arg Ser Leu His Gln Arg Ala Arg
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Ala
305

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<213> Sorangium cellulosum

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35 40 45

Lys Ala Arg Ala His Gly Ala Met Leu Gly Gly Arg Asp Asp Gly Trp
50 55 60

Arg Arg Gly Leu Pro Gly Ala Gly Ala Leu Arg Ala Ala Leu Gln Arg
65 70 75 80

Gly Arg Ser Arg Asp Leu Ala Arg Arg Arg Leu Ile Ala Ser Val Ser
85 90 95

Leu Ala Gly Gly Ala Ser Met Ala Val Val Ser Leu Phe Gln Leu Gly
100 105 110

Ile Ile Glu Arg Leu Pro Asp Pro Pro Leu Pro Gly Phe Asp Ser Ala
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Lys Val Thr Ser Ser Asp Ile
130 135

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pEPO15H2.7 end "A"

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cggtcagatc gacgacgggc tttcc 25

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(54) Title: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

(57) Abstract

Nucleic acid molecules are isolated from *Sorangium cellulosum* that encode polypeptides necessary for the biosynthesis of epothilone. Disclosed are methods for the production of epothilone in recombinant hosts transformed with the genes of the invention. In this manner, epothilone can be produced in quantities large enough to enable their purification and use in pharmaceutical formulations such as those for the treatment of cancer.

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INTERNATIONAL SEARCH REPORT

Inter nal Application No
PCT/EP 99/04171

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/52 C07K14/535 C07D493/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K C07D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 98 22461 A (BIOTECHNOLOG FORSCHUNG GMBH ;GERTH KLAUS (DE); HOEFLE GERHARD (DE)) 28 May 1998 (1998-05-28) the whole document	1-10
Y	SCHUPP T. ET AL.: "A Sorangium cellulosum (myxobacterium) gene cluster for the biosysnthesis of the macrolide antibiotic soraphen A: cloning, characterization and homology to polyketide synthase genes from actinomycetes" J. BACTERIOL., vol. 177, no. 13, 1995, pages 3673-3679, XP000893003 the whole document	1-10

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
17 April 2000	03/05/2000

Name and mailing address of the ISA	Authorized officer
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INTERNATIONAL SEARCH REPORT

Inter nal Application No
PCT/EP 99/04171

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
T	MOLNAR I. ET AL.: "The biosynthetic gene cluster for the microtubule-stabilizing agents epothilones A and B from Sorangium cellulosum So ce90" CHEM. BIOL., vol. 7, 2000, pages 97-109, XP000904734 the whole document	1-93
T	TANG LI, ET AL.: "Cloning and heterologous expression of the epothilone gene cluster." SCIENCE, vol. 287, 28 January 2000 (2000-01-28), pages 640-642, XP002135841 the whole document	1-93

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INTERNATIONAL SEARCH REPORT

information on patent family members

Inter nal Application No
PCT/EP 99/04171

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9822461 A	28-05-1998	AU 5483798 A	10-06-1998
		CN 1237970 A	08-12-1999
		CZ 9901750 A	15-09-1999
		EP 0941227 A	15-09-1999
		NO 992338 A	14-05-1999
		PL 333435 A	06-12-1999